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February 10, 2004, 16:18:30 ; Search time 11.5063 Seconds (without alignments) 731.761 Million cell updates/sec
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                                                                                                                                                  US-10-083-336A-5
1025
1 MIFPKQYPIINFTTAGATVQ......ARFQYIEGBMRTRIRYNRRS 199
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Patent No. 52
Sequence 16,
Sequence 61,
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Sequence 1,
Sequence 1,
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Sequence 7
Sequence 7
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(GGTZ 6/ptodata/1/iaa/5A COMB.pep:*
): /cgnZ 6/ptodata/1/iaa/5B-COMB.pep:*
// CGNZ 6/ptodata/1/iaa/6A-COMB.pep:*
// CGNZ 6/ptodata/1/iaa/6A-COMB.pep:*
// CGNZ 6/ptodata/1/iaa/PCTUS COMB.pep:*
// CGNZ 6/ptodata/1/iaa/PCTUS COMB.pep:*
// CGNZ 6/ptodata/1/iaa/PCTUS COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-338-793D-61
US-09-538-873-1
US-08-485-286-77
US-08-481138-6
US-08-477-484B-6
US-08-646-360-6
                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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US-07-988-430-1
US-08-425-336-1
US-08-447-4848-1
US-08-646-360-1
US-08-136-1
US-09-136-389-1
US-09-136-389-1
US-09-136-389-1
US-09-136-388-1
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US-08-485-286-27
5248606-4
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US-08-378-761A-74
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Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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0; Gaps

Length 268; Indels 0

Query Match 100.0%; Score 1025; DB 2; Best Local Similarity 100.0%; Pred. No. 6e-112; Matches 199; Conservative 0; Mismatches 0;

TYPE: amino acids
TOPOLOGY: 1100-

, MOLECULE TYPE: protein US-08-356-786-8

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VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEALTHLFTDVQNRYTFAF 120
                                                                                                                         61 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
                                                                                                                                                                       121 GGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 180
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  MIFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL
                                      1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL
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Best Local Similarity 100.0%; Pred. No. 1.7e-111;
Matches 199; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Pitcher, Edmund R. REGISTRATION NUMBER: 27,829
REPERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07/831,967
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08356786
Patent No. 5877305
                                                                                                                                                                                                                                                                                            181 RFOYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Huston, James S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/83
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          534 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-08-356-786-10
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61 VELSNHABELSVILALDVINAYVVGYRAGNSAYPFHPDNOEDAEAITHLFTDVQNRYTFAF 120

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APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
CORRESPONDENCE ADDRESS:
                                                GGNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAA 180
                                                                             63 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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99.5%; Score 1020; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two First National Plaza, 20 South Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 53765464nd, Greeta E.
REFERENCE/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
                                                                                                                                        181 RFQYIEGEMRIRIRYNRRS 199
                                                                                                                                                                                                                                                                             US-07-901-707-1
; Sequence 1, Application US/07901707
; Patent No. 5376546
; GENERAL INFORMATION:
; APPLICANT: Bernhard, Susan L.
                                                                                                                                                                                      183 RPOYIEGEMRTRIRYNRRS 201
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TELEPHONE: (312) 346-5750
TELEPAX: (312) 984-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-07-901-707-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Bicknell
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: USA
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Best Local Similarity
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                                                                                                                                                                                                                                APPLICANT: UTESTTA, ELLEN S.
APPLICANT: GARLEY GALEN S.
APPLICANT: GALESTE, UTCTOR F.
APPLICANT: GALESTE, UTCTOR F.
APPLICANT: GALESTE, TOWN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: COMPOSITIONS COMPOUNDS
FILE REPERENCE: UTSD: 884US
CURRENT FILING DATE: 2002-10-29
FRIOR RILING DATE: 2000-03-30
FRIOR PRILING DATE: 2000-03-30
FRIOR FILING DATE: 1999-03-30
FRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROME (VLS)
FILE REFERENCE: UTSD:603
CURRENT APPLICATION NUMBER: US/10/440,796
CURRENT FILING DATE: 2003-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ELSNHABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTOLPTLARSFIICIOMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MVPKQYPIINFTTAGAIVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 1019; DB 12; Length 267; Best Local Similarity 100.0%; Pred. No. 2.2e-108; Matches 198; Conservative 0; Mismatches 0; Indels 0;
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PRIOR APPLICATION NUMBER: US/09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
                                                                                                   RESULT 2
US-10-282-935-1
; Sequence 1, Application US/10282935
; Publication Net US20030143193A1

Publication Net US20030143193A1
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Publication No. US20040009148A1
GENERAL INFORMATION:
181 FQYIEGEMRTRIRYNRRS 198
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 BLSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michel P
APPLICANT: Byrne, Michel P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                               100.0%; Score 1019; DB 12; Length 267; 100.0%; Pred. No. 2.2e-108; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
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99.1%; Score 1010; DB 12;
Best Local Similarity 100.0%; Pred. No. 1.5e-107;
Matches 196; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
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                                                                                                                    ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0
Matches 198; Conservative
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SOFTWARE: Patentin Ver. 2.1
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US-10-083-336A-3
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                            SEQ ID NO 1
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Best Local Similarity 100.0%; Pred. No. 2.2e-112; Matches 200; Conservative 0; Mismatches 0;
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                                                           February 10, 2004, 16:18:30; Search time 11.5641 Seconds (without alignments) 731.761 Million cell updates/sec
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                                                                                                                         1 MIFPKQYPIINFTTAGATVQ......RFQYIEGEMRTRIRYNRRSA 200
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Patent No. 5
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-485-286-77
US-08-488-113B-6
US-08-477-484B-6
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US-08-356-786-10
US-07-9910-707-1
US-07-9910-707-1
US-08-425-336-1
US-08-488-113B-1
US-08-46-360-1
US-08-646-360-1
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US-08-646-360-1
US-09-610-838-1
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US-08-338-793D-61
US-09-538-873-1
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US-08-485-286-27
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Maximum Match 100%
Listing first 45 summaries
                                         - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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8 342 33.2 267 1 119-08-485-286-74 Semience 74	US-07-923-692C-4 Sequence 4, US-08-184-237-4 Sequence 4,	2 342 33.2 289 3 US-08-484-341-4 Sequence 4, 342 33.2 289 3 US-08-484-341-4 Sequence 6, 3 342 33.2 289 3 US-08-483-502-4	4 342 33.2 289 4 US-09-726-651A-4 Sequence 4, 5 341.5 33.2 289 1 HS-08-324-301-15 Sequence 16	6 329.5 32.0 250 1 US-08-378-761A-71 Sequence 71,	8 323.5 31.4 251 4 US-09-538-873-3 Sequence 3,	9 312.5 30.4 255 1 US-07-901-707-6 0 312.5 30.4 255 1 US-07-988-430-6	1 312.5 30.4 255 1 US-08-425-336-6 Sequence 6,	2 312.5 30.4 255 5 PCT-US92-09487-6 Sequence 6, 3 312 30.3 248 3 US-08-902-486-7 Sequence 7.	4 312 30.3 290 1 US-08-245-754A-2 Sequence 2,	Sequence ST. CONMENTED Sequence	CTARTINGTER	١.	786-8	; Sequence B, Application US/08356786 ; Parent No. 5877305	AL INFORMATION:	şΑİ	rid B. Biogeophychia Bindina protein for	; IIILE OF INVENTION: BIOSYNCHETIC BINGING Frotein for Cancer ; TITLE OF INVENTION: Marker	NUMBER OF SEQUENCES: 16	SS: R. Ditcher	: Exchange Place, 53 State Street	STATE: Massachusetts	; ZIP: 02109	ER READABLE FORM	E: Flor	; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS	lease	ľ	, occ /oc /oc	; CLASSIFICATION: 424	FALCATION DATA	ú	; ATTORNEY/AGENT INFORMATION:	REGISTRATION NUMBER: 27,829	TELECOMMUNICATION INFORMATION:	(617) 24	; INPORMATION FOR SEQ ID NO: 8:	; SEQUENCE CHARACIERISTICS; : LENGTH: 268 amino acida	TYPE: amino acid	MOLECULE	US-08-356-786-8	h 100.0%; Score 1029; DB 2	
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APPLICANT: Berthard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
CORRESPONDENCE ADDRESS:
                                            GGNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 180
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                                                                                           123 GGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 182
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63 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two First National Plaza, 20 South Clark STREET: Street
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CURRENT APPLICATION DATA:
CURLENTON NUMBER: US/07/901,707
FILING DATE: 19920619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
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                                                                                                                                       181 RFQYIEGEMRTRIRYNRRSA 200
                                                                                                                                                                  183 RFQYIEGEMRIRIRYNRRSA 202
                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/07901707; Patent No. 5376546
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(312) 984-5750
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0
Matches 199; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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OPERATING SYSTEM:
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Illinois
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                                                                                                                                                                                 61 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
                                                                                        61 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
                                                                                                                        61 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
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                             1 MIFPKQYPIINFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL 60
MIPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: APPLICANT: ALOUS DAVIG B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 424
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            181 RFQYIEGEMRTRIRYNRRSA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08356786
Patent No. 5877305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Pitcher, Edmund R. REGISTRAITON NUMBER: 27,829 REFERENCE/DOCKET NUMBER: CRETELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INPORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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Query Match

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein February 10, 2004, 16:17:35 ; Search time 10.7687 Seconds Run on:

(without alignments) 1777.145 Million cell updates/sec

US-10-083-336A-5 1025 Title: Perfect score:

1 MIFPKQYPIINFTTAGATVQ......ARFQYIEGEMRTRIRYNRRS 199 Sequence:

Scoring table:

283308 seqs, 96168682 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 76:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	ricin D precursor	tin	abrin-d precursor				karasurin - Mongol	-B	- 1	ne 7		beta-luffin - smoo	SE	addlutinin I precu	mistletoe lectin I	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-qlycosidase		rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	antiviral protein	>		rRNA N-glycosidase	rRNA N-glycosidase	tritin - wheat
ΩI	RLCSD	RLCSAG	532431	S16022	S32430	RLTZT	JU0393	JC5032	JC5606	C39761	TZLSA	823519	3N0108	862627	PD0018	522494	825560	JC4840	RLPUGG	JC4235	JT0753	S28421	S17757	JE0401	A3981.7	JC4811	T12573	RLBH	833631
DB	Н	П	7	~	7	Н	7	7	7	7	Н	7	71	~	7	~1	~	7	Н	7	7	7	N	7	7	7	7	Н	7
Length	576	564	528	562	527	289	247	247	289	251	528	278	250	570	254	277	286	245	286	286	316	294	313	261	278	272	289	280	275
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30K ribosome inact	protein synthesis	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	ribosome-inactivat	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-qlycosidase	rRNA N-qlycosidase	shiga-like toxin I	Shiga toxin 2 subu	Shiga toxin 2 subu	Shiga-like toxin I	rRNA N-glycosidase
B38664	JC5848	S28542	\$28539	S29931	S46239	805205	S17519	S28541	RLQHG2	A58923	154695	E90779	G85640	801032	S17932
7	7	N	~	7	N	7	7	7	Н	7	7	7	~	N	0
281	280	253	253	253	310	283	293	253	292	253	319	319	319	318	236
13.0	12.9	12.8	12.4	12.4	12.3	12.1	12.0	12.0	11.8	11.2	10.8	10.8	10.8	10.8	10.7
133	132	131	127	127	126	124	123.5	123	121	115	111	111	111	110.5	110
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	4 5

ALIGNMENTS

RESULT 1

RLCSD
ricin D precursor - castor bean
N; Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R; Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A; Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A; Reference number: A24041; MUID:86067214; PMID:2999712
A; Accession: A24041
A; Molecule type: DNA
A;Residues: 1-576 <hal></hal>
A; Cross-references: GB: X03179; NID: q21082; PIDN: CAA26939.1; PID: q21083
R,Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A; Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene &
A; Reference number: S20513; MUID:92163016; PMID:1371405
A;Accession: S20513
N. Mollowill transfer Park

A;Molecule type: DNA A;Residues: 1-576 <TRE>

A;Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085.R;Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Blochem. 148, 265-270, 1985.
A;Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A;Reference number: A24614; MUID:85179479; PMID:3838723
A;Accession: A24614

A,Molecule type: mRNA A,Residues: 12-75, D',77-550, R',552-576 <LAM> A,Residues: 12-75, D',77-550, R', 552-576 <LAM> A,Coss-references: GB.X02388, NID:g21077; PIDN:CAA26230.1; PID:g21078 R,Yoshitake, S.; Funatsu, G.; Funatsu, M. Agric. Biol. Chem. 42, 1267-1274, 1978 A,Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile challs. A,Reference number: A03372 A,Reference number: A03372

A; Molecule type: protein https://doi.org/10.272-283,/L',285-288,290-302 < YOS> A; Residues: 36-97,/Q',99-109,'S',111-269,'D',272-283,'L',285-288,290-302 < YOS> A; Note: this paper cites the others in the series providing experimental details for the R; Araki, T.; Funatsu, G. R: Araki, T.; Funatsu, G. FEBS Lett. 191, 121-124, 1985 A; FIELE: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan A; Reference number: A24010

A;Accession: A24010

A; Molecule type: protein A; Residues: 315-383, PS', 386-576 cARA> A; Residues: 315-383, PS', 386-576 cARA> A; Funatsu, G.; Kimura, M.; Funatsu, M. Agric. Biol. Chem. 43, 2221-2224, 1979 A; Tile: Primary structure of Ala chain of ricin D. A; Reference number: A03374 A; Accession: A03374 A; Molecule type: protein

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A, Residues: 315-335, 'N', 337-342, 'NH', 345-362, 364-383, 'PS', 386-399, 'T', 401, 'D', 403, 'E', 40  
527, 'E', 529-564, 'W', 566, 'H', 567-570, 'LI', 573-574, 'F' < FUNS  
A,Note: this paper, one of a series, summarizes the experimental details for the determinence of a series, summarizes the experimental details for the determinence of a series, Jub.

Proteins 10, 270-278, 1991
A,Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of A,Reference number: A48231 MUID: 91352006; PMID: 1881883
A,Contents: annotation, active site
R,Rutenber, E.; Robertus, Jub.
Proteins 10, 260-269, 1991
A,Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A,Reference number: A48238; MUID: 91352005; PMID: 1881882
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C.Species: Ricinus communis (castor bean)
C.Species: Ricinus communis (castor bean)
C.Species: Nicontains: A24261; A82410
R.Shocersion: A24261; A24210
R.Shoberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J. Biol. Chem. 260, 15682-15686, 1985
A.Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin. A.Reference number: A24261; MUID:86059449; PMID:2999130
A.Rocesion: A24261
A.Molecule type: mRNA
A.Rocesion: 1-564 RNDS
A.Rocesion: BNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
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Matches 198; Conserv
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A; Molecule type: protein
has strong agglutinating activity and weak cytotoxicity compared
C; Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C; Superfamily: ricin; rRNA N-glycosidase homology kydrolase; lectin; RNA binding; seed
F; 1-24/Domain: signal sequence #status predicted &SIG>
F; 25-290/Product: agglutinin chain A #status predicted &ACH>
F; 35-291/Domain: rRNA N-glycosidase homology «RNG>
F; 35-291/Domain: rRNA N-glycosidase homology «RNG>
F; 35-291/Domain: signal sequence #status experimental &BCH>
F; 319-364, 352-405-444, 450-485, 490-528, 531-564/Region: 40-residue repeats
F; 319-364, 332-405-443, 450-485, 490-528, 531-564/Region: 40-residue repeats
F; 34, 259/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 3200, 203/Active site: Glu, Arg #status predicted
F; 282-306, 232-341, 365-382, 453-666, 492-509/Disulfied bonds: #status predicted
F; 282-306, 232-341, 265-382, 453-666, 492-509/Disulfied bonds: #status predicted
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F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;261-528/Product: abrin-d chain B #status predicted <BCH>
R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophyr. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti!
A;Reference number: A24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;324,337,348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted F;397,437/Binding site: carbohydrate (Asn) (covalent) #status experimental F;536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 IFPKQYPIINFTTADATVESYTNFIRAVRSHLTTGADVRHEIPVLPNRVGLPISQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 930.5; DB 1; Length 564; Pred. No. 5.6e-76; 7; Mismatches 8; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                abrin-d precursor - Indian licorice (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N, Contains: rRNA N-glycosidase (EC 3.2.2.22)
C, Species: Abrus precatorius (Indian licorice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 FQYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 FQYIEGEMRTRIRYNRRS 221
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Best Local Similarity 91.94
Matches 182; Conservative
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A;Cross-references: GB:M98346
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A; Residues: 1-528 <HUN>
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A.Molecule type: protein
A.Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430,
A.Experimental source: seed
A.Experimental source: seed
C.Superfamily: ricin; rRNA N-glycosidase homology
C.Superfamily: ricin; rRNA N-glycosidase homology
C.Superfamily: ricin; rRNA N-glycosidase homology
C.Steywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; py
F): 250/Product: abrin-b chain B #status predicted <ACH>
F): 260-527/Product: abrin-b chain B #status experimental <BCH>
F): 282-324, 335-365, 368-406, 413-484, 452-491, 494-527/Region: Predicted
F): 10, 360, 460 Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F): 10, 360, 460 Binding site: carbohydrate (Asn) (covalent) #status predicted
F): 163, 166/Active site: Glu, Arg #status predicted
F): 268, 268, 268, 285-304, 328-345, 416-429, 455-472/Disulfide bonds: #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Cross-references: GB:M98345; NID:gl66296; PIDN:AAA32625.1; PID:gl66297
R.Kimura, M.; Sumizawa, T.; Funatsu, G.
Bisci. Biotechnol. Biochem. S7, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic A;Reference number: JC1398; MUID:93169023; PMID:7763422
                                                                                149 DLERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYI 205
                                          126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 30-Sep.1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: $32430; JC1399
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
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                                                                                                                                                                                                                                                            206 SNRVGVSIR 214
                                                                                                                                                                                           186 EGEMRTRIR 194
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Best Local Similarity
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Bur. J. Biochem. 198, 723-732, 1991
A;Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chai A;Reference number: S16022; MUID:91266957; PMID:2050149
A;Accession: S16022
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                              F;1/Modified site: pyrrolidone carboxylic acid (Gin) #status predicted
F;74,113,195,196/Bhidding site: subbstrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;286,365,353,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;286,312/Binding site: N-acety/galactosamine (Asp, Asn) #status predicted
F;500,521/Binding site: N-acety/galactosamine (Asp, Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFGGNYD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 SERESIEVGIDVINAYVVAYRAGSQSYFL---RDAPASASIYLFPGTQ-RYSLRFDGSYG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
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F;283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
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C;Species: Abrus precatorius (Indian licorice)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 QDQVIKFTTBGATSQSYKQFIBALRQRLTGG--LIHDIPVLPDPTTVEERNRYITVELSN
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A;Residues: 1-562 <WOO>
A;Cross-references: EMBL:X55667; NID:g16084; PIDN:CAA39202.1; PID:g16085
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                                                                                                                                                                                                                                                                                                                         ; Score 353.5; DB 2; Length 528;
; Pred. No. 5.2e-24;
24; Mismatches 70; Indels 9
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45.5%;
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4
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                                                                                                                                                                                                                                                                           66 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYIFAFGGNYD 125
                                                                                                                                                                                                                                                                                                                                                                  59 SDTESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                     1 ODOVIKETTEGATSOSYKOFIEALRORLTGG--LIHGIPVLPDPTTLOERNRYISVELSN 58
                                                                                            6 QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rRNA N-glycosidase (EC 3.2.2.2) alpha-trichosanthin precursor [validated] N;Alternate names: alpha-TCS; type I ribosome-inactivating protein C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
10; Gaps
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C,Accession: GC5032
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Rilondo, T.; Mizukami, H.; Takeda, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of Karasurin-B and Ka A;Reference number: JC5032; MUID:97108848; PMID:8951169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: TU0393; PS0163
K:TOYOkawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin.
A;Reference number: JU0393; WUID:92005921; PMID:1914000
                                                                                                                                                                                                                                                                                                           S2 TISVAIDVTNVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPPSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 IISVAIDVINVYWGYRAGDISYFF---NEASATEAAKYVFKDAKRKVTLPPSGNXERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                    129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
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C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequance_revision 30-Sep-1991 #text_change 12-Apr-1995
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C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
                                                                                                                10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                    SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
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                                              Indels
2.6e-23;
ches 54;
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                                          Mismatches
       Pred. No.
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39.5%;
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                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-247 <TOY>
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A; Molecule type: protein
A; Residues: 1-247 < KON>
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   Best Local Similarity
Matches 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: JU0393
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A, Molecule type: protein
A; Residues: 24-270 (COL)
R; Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
R; Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pure Appl. Chem. 58, 789-798, 1986
A; Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
A; Reference number: JT0003
A; Molecule type: protein
A; Residues: 24-56, L', 58-59, I', 61-71, I', 73-81,85-86, L', 88-92, DAGLPRNAVL', 93-142, GL'
A; Experimental source: tuber
R; Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A; Reference number: A67091; PDB:LNRJ
A; Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-84; Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
Submitted to the Brookhaven Protein Data Bank, July 1994
A; Reference number: A67092; PDB:LNRZ
A; Reference number: A67092; PDB:LNRZ
A; Reference number: A67092; PDB:LNRZ
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B, Reference number: A66711; PDB:11CS
B, Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27 R; Xiong, J.P.; Xia, Z.X.; Wang, Y. Nat. Struct. Biol. 1, 695-700, 1994
B, Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution ref
                                                                                                                                                                                                                                                 A; Mcceule type: mRNA
A; Residues: 1-289 <SHA>
A; Residues: 1-289 <SHA>
A; Cross.references: GB HAS
A; Cross.references: GB HAS
A; Cross.references: GB HAS
A; Cross.references: GB HAS
A; Experimental source: tuber
B; Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A; Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rib
A; Reference number: A36274; MUID:90256790; PMID:2341400
A; Accession: A36274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-72, VV, 74-90, S, 92-233, Tr, 235-267, D, 269-289 <ZHE>
A,Kresidues: 1-72, VV, 74-90, S, 92-233, Tr, 235-267, D, 269-289 <ZHE>
A,Cross-references: GB:S70176; NID:g547148; PIDN:AAB31048.1; PID:g547149
R,Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
B, Blol. Chem. 265, 8665, 1990
A,Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abr
A,Reference number: A36273; MUID:90256789; PMID:2341399
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C;Date: 30-Sep-1988 #sequence_revision 26-Jan-1996 #text_change 23-Mar-2001 C;Accession: JT0566; A36274; JC1093; A36273; JT0003 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W. Gene 97, 267-272, 1991 A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli. A;Reference number: JT0566; MUID:91153657; PMID:1999291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-233, T',235-246, M',248-289 cCHO>
A; Cross-references: GB: U05444; NID: g170534; PIDN: AAA34206.1; PID: g170535
R; Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
Acta Genet. Sin. 21, 42-51, 1994
A; Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A; Reference number: UC1093; MUID: 94271613; PMID: 8003348
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A;Contents: annotation; X-ray crystallography, 1.7 angstroms
                                                                                                                                                                                                                             A; Accession: JT0566
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A'Accession: S32429
A,Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83; Conservative
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                194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 RTRIR 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 'M', 1-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
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A;Cross-references: DDBJ:AB000666; NID:g2329830; PIDN:BAA21786.1; PID:g2329831
A;Croso, T; Mizukami, H:, Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 148-1489, 1986
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
A;Reference number: UC5032; MUID:97108848; PMID:8951169
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N; Contrains: karasurin A (Species: Trichosambes kirilowii var. japonica (Species: Trichosoma, UC5606; UC5033 (Species: V. Rondo, T.; Ogihara, Y. Rilan, Bull. 20, 711-713, 1997 (Species: V. Rondo, T.; Ogihara, V. Raman, Bull. 20, 711-713, 1997 (Species: V. Raman, Bull. 20, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;22-270/Product: karasurin C #status predicted <AMAC>
F;24-270/Product: karasurin A #status predicted <AMAC>
F;27-266/Domain: rRNA N-glycosidase homology <RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 IISVAIDVINVYVMGYRAGDISYFF---NEASAIEAAXXVFKDAKKKVTLPYSGNYERLO 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVILALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
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                                                                                                                                                                                                                                                                                                                                                          2 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHITHYADE
                                                                                                                                                                                                                                                                                                             10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                               Length 247;
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40.0%; Pred. No. 5.9e-23;
tive 46; Mismatches 53; Indels
                                                                                                                                                                                                                                        53; Indels
                                                                                                                                                      33.0%; Score 338; DB 2;
40.0%; Pred. No. 4.9e-23;
tive 46; Mismatches 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   karasurin C - Tríchosanthes kirilowii var. japonica
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A.Molecule type: protein
A.Residues: 22-270 <KON>
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                                                                                                                                                                                           Local Similarity
tes 74; Conserv
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171 IGKRV 175
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Best Local S
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N; Contains: rRNA N-glycosidase (EC 3.2.2.2)
C; Species: Abrus precatorius (Indian licorice)
C; Species: Abrus precatorius (Indian licorice)
C; Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #text_change 16-Jul-1999
C; Accession: S32429; U70202; A39761; U01398; S14472; S24133; S74110; S74111
R; Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol, 229, 263-267, 1993
A; Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Cor-A; Reference number: S32429; MUID:93132798; PMID:8421313
                                     N; Contains: rRNA N-grycosidase (EC 3.12.22)
(s) Species: Abrus precatorius (Indian licorice)
(c) Species: Abrus precatorius (Indian licorice)
(c) Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
(c) Accession: (239761; 814471
(R) Evensen, G.; Mathiesen, A.; Sundan, A.
(b) Biol. (Chem. 266, 6848-86852, 1991
(A) Hitle: Direct molecular cloning and expression of two distinct abrin A-chains.
(A) Reference number: A39761; MUID:91201329; PMID:2016300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C.Superfamally: ridin; KTNA N-glycosidase homology
C.Superfamally: ridin; KTNA N-glycosidase; hydrolase; lectin; toxin
F:1-251/Product: abrin (clone 7.2) chain A #status predicted AACH>
F:7-246/Domain: RTNA N-glycosidase homology <RNG>
F:7-446/Domain: RTNA N-glycosidase homology <RNG>
F:74.113,195,196/Binding site: substrate (Tyr, Glu, Asn) #status predicted
F:164,167/Active site: Glu, Arg #status predicted
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A; Residues: 'E', 2-528 <hr/>
A; Residues: 'E', 2-528 <hr/>
A; Cross-references: GB: M98344; NID: 9166294; PIDN: AAA32624.1; PID: 9166295
A; Note: the coding region for the sequence shown is preceded by an ATG codon
A; Note: residues 1-8 were derived from the synthesized primer
R; Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-251 <BVE>
R;Pvensen, G; Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
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abrin (clone 7.2) precursor - Indian licorice (fragment)
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C;Species: Luffa cylindrica (smooth loofah)
C;Species: Luffa cylindrica (smooth loofah)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
C;Accession: 823519; 823113
R;Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
R;Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
R;Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
A;Title: Nuclectide sequence of cpNA encoding beta-luffin, another ribosome-inactivating
A;Reference number: 823519; MUID:92353400; PMID:1643290
                                                                                                                                                                          70 SVTLALDVINAYVVGYRACNSAYFFH--PDNQEDAEAITHLFIDVQNRYTFAFGGNYDRL 127
                                                                                                                                                                                                                                                                                                                                                    128 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 187
                                                                                                                                                                                                                                                                                                                                                                                                      10 INFITAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
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35.8%; Pred. No. 3.2e-20;
cive 45; Mismatches 64
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Matches 67; Conservative
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A,Molecule type: protein
A,Residues: 1-250 <ISL>
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A; Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from sheerence number: JT0202
A; Reference number: JT0202
A; Molecule type: protein
A; Molecule type: protein
A; Rolecule type: Drotein
A; Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
B; Evensen, G: Mathiesen, A: Sundan, A.
A; Ditle: Direct molecular cloning and expression of two distinct abrin A-chains.
A; Reference number: A39761; MUID:91201329; PMID:2016300
A; Reference number: A39761; MUID:91201329; PMID:2016300
A; Reference number: Bay MuiD:91201329; PMID:2016300
A; Reference number: Bay Molecule type: DNA
A; Residues: 'E', 2-251 ckWs
A; Residues: 'E', 2-2
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Cisuperfamily: ricin; rRNA N-glycosidase homology
Cikeywords: duplication; glycosidase; hydrolase; lectin; pyroglutamic acid F;7-246/Domain: rRNA N-glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid F;7-246/Domain: rRNA N-glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid F;7-246/Domain: rRNA N-glycoprotein; B status experimental <BCH>
F;283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;14,113,195,196/Bunding site: substrate (Tyr, Tyr, Glu, Ann) #status predicted
F;247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
F;288-312/Binding site: N-acetylgalaccosamine (Asp, Asn) #status predicted
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A, Molecule type: protein
A, Residues: 262-297, Y'. 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 < CHE>
R, Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Bir. J. Blochem. 240, 564-569, 1996
A, Title: Probing the domain structure of abrin-a by tryptic digestion.
A; Reference number: 874110; MUID:97008945; PMID:8856055
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A; Accession: S14472
A; Status: preliminary
A; Molecule type: DNA
A; Escidues: 'ME', 2-251 < EV2>
A; Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
A; Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
B; Chen, Yi.; Chow, L.P.; Tsugita, A.; Lin, J.Y.
FEBS Lett. 309, 115-118, 1922
A; Title: The complete primary structure of abrin-a B chain.
A; Reference number: S24133; MUID:92371656; PMID:1505674
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A, Accession: 101398
A; Molecule type: protein
A; Residues: 261-347, Tr,349-351,'A',353-357,'L',359-528 «KIM»
A; Experimental source: seed
B; Evensen, G; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A; Description: Direct molecular cloning of two distinct abrin A-chains.
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A;Residues: 262-276,'X',278-280;329-348;369-388;399-418 <LIW>
A;Experimental source: seed
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A; Residues: 89-108;154-172 <LIN>
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Best Local Similarity
Matches 80; Conserv
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C;Accession: UN0108
R;Islam, M.R.; Hirayama, H.; Funatsu, G.
Rapic. Biol. Chem. 55, 229-238, 1991
A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from A;Reference number: UN0108; MUID:91248488; PMID:1368666
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C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                24 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK
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A;Cross-references: EMBL:X62372; NID:g19149; PIDN:CAA44230.1; PID:g19150
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;26-264/Domain: rRNA N-glycosidase homology <RNG>
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Search completed: February 10, 2004, 16:28:01
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(Species: Viscum album

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                                                                48; Mismatches 64; Indels
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34.2%; Pred. No. 1.2e-19;
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A.Residues: 29-39;309-319 <VA2>
C;Superfamily: ricin; rRNA N-glycosidase homology
F;37-283/Domain: rRNA N-glycosidase homology <RNG>
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A;Residues: 1-570 <VAN>
Best Local Similarity
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67 TAAIDVINAYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 122
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                                                                                                                                                                                                                                                                                                                                                                         9 THQTTGEEYPRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGQDSV 66
                                                                                                                                                                                                                                                                                                                                  14 TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV 71
                                                                                                                                                                                                                                                            56; Indels 38; Gaps
                                                                                                                                                                                                    Length 254;
                                                                                                                                                                                             Query Match 27.9%; Score 286; DB 2; Best Local Similarity 38.4%; Pred. No. 2.4e-18; Matches 81; Conservative 36; Mismatches 56;
                            A;Molecule type: protein
A;Residues: 1-254 cBCC.
C;Superfamily: ricin; rRNA N-glycosidase homology
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GEMRTRIRYN 196
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A; Accession: PD0018
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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 10, 2004, 16:13:55; Search time 6.63825 Seconds (without alignments) 1409.756 Million cell updates/sec Run on:

US-10-083-336A-5 1025 1 MIFPKQYPIINFTTAGATVQ......ARFQYIEGEMRTRIRYNRRS 199 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 Total number of hits satisfying chosen parameters:

127863 segs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Length	DB	ID	escri
1	102	6	5	٦	IC	įΉ
7	930.5	90.8	564	Н	AGGL_RICCO	ໝ
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9	341.5	ë,	282	Н	RIP2_BRYDI	P98184 bryonia dio
7	338	33.0	289	Н	RIPS TRIKI	
ω	330.5	ď	563	Н		m
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10	312	o.	290	Н	RIP1_BRYDI	bryon
11	300.5	9.	250	Н	RIPB_LUFCY	luffa c
12	296.5	8	286	Н	RIP1 CUCFI	cucum
13	286	7	254	Н	MLA VISAL	viscum
14	284.5	7	277	Н	RIPA LUFCY	luffa
15	279	7.	286	щ	RIP2 MOMBA	P29339 momordica b
16	277	27.0	286	Н	RIP1 MOMCH	P16094 momordica c
17	260	25.4	294	Н		
18	242.5	m.	316	Н	RIPG GELMU	
19	197.5	6	294	Н	RIPA PHYAM	
20	182	17.8	313	ч	RIP1 PHYAM	7
21	180.5	17.6	261	٦	RIPS PHYAM	
22	175		278	-	RIPP MIRJA	P21326 mirabilis j
23	140	•	280	Н	RIP2 HORVU	
24	133	13.0	280	Н	RIP1 HORVU	P22244 hordeum vul
25	131		253	-4	RIP7 SAPOF	Q41391 saponaria o
56	127	•	253	Н	RIPS SAPOF	Q41389 saponaria o
27	126	•	310	٦	RIP2 PHYAM	. 27
28	124	•	299	Н	RIP6 SAPOF	
29	123.5		293	Н	RIPO DIACA	P24476 dianthus ca
30	121		292	Н	RIP2 SAPOF	P27559 saponaria o
31	111	10.8	319	Н	SLTA_BP933	35
32	110	•	236	Н	ارا	0 sapo
33	109.5	10.7	300	Н	RIP3 MAIZE	391 z

P28522 zea mays (m	P25892 zea mays (m	Q00531 hordeum vul	P08026 bacteriopha	P10149 bacteriopha	067411 aquifex aeo	083746 treponema p	P09166 aeromonas t	P75255 mycoplasma	•••	P09167 aeromonas h	P27561 saponaria o
PX MAIZE	P9 MAIZE	:60_HORVU	TA_BPH19	SLTA_BPH30	TV AQUAE	SH TREPA	RA_AERTR	148 MYCPN	RS_AERHY	RA AERHY	P4_SAPOF
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7.5	103	102	91	16	85.5	85	82.5	81	78.5	78.5	92
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ALIGNMENTS

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**Xin Y., Robertus J.D.;

"Analysis of several key active site residues of ricin A chain by
"Analysis of several key active site residues of ricin A chain by
mutagenesis and X-ray crystallography.";

"Drotein Eng. 5:775-779(1992).

"I protein Eng. 5:775-779(1992).

"I protein Eng. 5:775-779(1992).

"I protein Eng. 5:775-779(1992).

"I protein Eng. 5:775-779(1992).

"I constant colland tells and cells and to a less extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 608 inbookers as a glycosidase that removes a specific adenine residue from an exposed loop of 28s ribosomal RAM. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to call receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agolithming the cell agolithming the cell of the A chain; B chains are also responsible for contractive and animal cell of the A chain; B chains are also responsible cell agolithming to cell agolithming to cell agolithming the cell of the A chain; B chains are also responsible cell agolithming the cell agolithming to cell agolithming the cell of the cell agolithming the cell of t
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SUBDIAT: Disulfide-linked dimer of A and B chains.

DOMAIN: The B chain is composed of two domains, each consists of 3 homologue subdomains (alpha, beta, gamma).

PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOWE-INACTIVATING PROTEIN FAMILY: TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             galactopyranoside moieties.
CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at
                                                                                          MEDLINE=87165983; PubMed=3558397;
Monfoort W. Villafranca O.B., Monzingo A.F., Ernst S.R., Katzin B.,
Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.;
"The three-dimensional structure of ricin at 2.8 A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Day P.J., Ernst S.R., Frankel A.B., Monzingo A.F., Pascal J.M., Molina-Svinth M.C., Robertus J.D., "Structure and activity of an active site substitution of ricin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
MEDLINE=97240820; PubMed=9086280;
Yan X., Hollis I., Svinth M., Day P., Monzingo A.F., Milne G.W.,
Robertus J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95082010; PubMed=7990130;
Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,
Pauptit R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
MEDLINE=96374222; PubMed=8780513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure-based identification of a ricin inhibitor."; J. Mol. Biol. 266:1043-1049(1997).
                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN. MEDLINE=91352005; PubMed=1881882; MEDLINE=91352005. Robertus J.D.; Robertus J.D.; Rictaber E., Robertus J.D.; Rictucture of ricin B-chain at 2.5-A resolution."; Proteins 10:260-269(1991).
                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. MEDLINE=91352004; PubMed=1881881; Katzin B.J., Collins B.J., Robertus J.D.; Structure of ricin A-chain at 2.5 A."; Proteins 10:251-259(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
                                                                     K-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                              Biol. Chem. 262:5398-5403(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 35:11098-11103(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93165632; PubMed=1287657;
"Ricin.";
Toxicon 39:1723-1728(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUTAGENESIS
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. ..).
/FTId=CRR 000080.
N-LINKED (GLCNAC. ..) (IN MINOR FORM).
/FTId=CRR 000081.
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
E -> D (IN REF. 3).
A -> R (IN REF. 3).
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
-!- CAUTION: REF.4 AND REF.5 SROUBNCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
-!- DATABASE: NAME=Protein Spotlight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSTE; PS50231, RICIN B LECTIN; 2.
PROSTE; PS50231, STICN B LECTIN; 1.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase, Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal; 3D-structure.
1 35.
                                                                            NOTE=Issue 31 of February 2003;
WWW="http://www.expasy.org/spotlight/articles/sptlt031.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               넊성
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RICIN B-TYPE LECTIN
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LINKER PEPTIDE
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PDB; 11L9; 16-JAN-02.
GlycoSuiteDB; P02879; -
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PP00652; Ricin_B_lectin, 6.
Pfam; PF00161; RIP; 1.
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EMBL, X52908; CAA37095.1; -.
EMBL, X02388; CAA26230.1; -.
EMBL, A12892; CAA01058.1; -.
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SMART; SM00458; RICIN; 2.
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1APG, 31-JAN-94.
1FRP, 31-OCT-93.
1IFR, 14-JAN-98.
1IFT, 14-JAN-98.
1IFU, 14-JAN-98.
1RTC, 31-OCT-93.
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02-SEP-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                    156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                      96 ELSNHAELSVILALDVINAYVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                         122 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAAR 181
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Lin T.T.-S., Li S.S.-L.;
Lin T.T.-S., Li S.S.-S., Li S.S., L
                                                                                                                                                                                                                                                         62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
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MEDLINE=8662949; PubMed=2999130;
REDLINE=8662949; PubMed=2999130;
REDERTS L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
"The primary sequence of Ricinus communis agglutinin. Comparison with
                                                                                                                                                                                         36 IFPKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Araki T., Yoshioka Y., Funatsu G.; The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."; Biochim. Biochys. Acta 872:277-285 (1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (BC 3.2.2.22); Agglutinin B chain].
Ricinus communis (Castor bean)
                                                            °;
Length 576;
                                                                Indels
99.5%; Score 1020; DB 1;
100.0%; Pred. No. 2.7e-87;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOYIEGEMRIRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 FOYIEGEMRIRIRYNRRS 233
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EMBL; S40368; AAB22584.1; -.
                                                                      Matches 198; Conservative
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                                     Similarity
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P06750;
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   Query Match
                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 ELSNHAELSVTLALDVTNAYVVGCRAGNSAYFFHPDNQEDAEAITHLFTDVQNSFTFARG
                                                                     PRINTS, PRO0196; SHIGARICIN.
SMART, SM00458; RICIN, 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.
1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 IFPKQYPIINFTTADATVESYTNFIRAVRSHLTTGADVRHEIPVLPNRVGLPISQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 41, Last annotation update)
Abrin-c precursor [Contains: Abrin-c A chain (rRNA N-glycosidase)
(EC 3.2.2.22); Abrin-c B chain].
Abrus precatorius (Indian licorice) (Crab's eye).
                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 564;
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                                                                                                                                                                                                                                                                                                  INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               D455F2A72F609759 CRC64;
                                                                                                                                                  AGGLUTINIA A CHAIN.
LINKER PEBPIDE.
AGGLUTININ B CHAIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 930.5; DB 1;
Pred. No. 5.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                       F -> T (IN REF. 2).

N -> D (IN REF. 2).

R -> G (IN REF. 2).

F -> V (IN REF. 2).

F -> V (IN REF. 2).
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BY SIMILARITY.
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N-LINKED
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2-ALPHA.
                              InterPro; IPR000772; Ricin_B_lectin.
InterPro; IRR001574; RIP.
Edm.; PR00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                 1-BETA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62851 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 90.8%;
Best Local Similarity 91.9%;
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
         HSSP; P02879; 1BR6.
GlycoSuiteDB; P06750;
                                                                                                                                                                                                                                                                                                                                                                                                                              374
404
552
564 AA;
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P28590;
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The Mood K.A., Lord J.M., Wawrzynczak B.J., Piatak M.,

"Preproabrin: genomic cloning, characterisation and the expression of
the A-chain in Becherichia coli.",

"Breproabrin: genomic cloning, characterisation and the expression of
the A-chain in Becherichia coli.",

"I Biochem. 198:773-773 [1991].

-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN

SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
SUBDINITS BY REMOVING ADBINITS FROM POSITION 4,324 OF 28 STRNA. THE
B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAY FACILITATES THE
BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-91ycosidic bond at one
specific adenosine on the 28S FRNA.

-!- CHAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN

CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).

-!- SIMILARITY: IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-
INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions a long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                          ong as its content is in no way oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabalés; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABRIN C A CHAIN (BY SIMILARITY).
LINKER PEPTIDE (BY SIMILARITY).
ABRIN C B CHAIN (BY SIMILARITY).
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
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INTERCHAIN (BY SIMILARITY).
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or send an email to license@isb-sib.ch).
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2-ALPHA.
2-BETA.
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InterPro; IPR001574; RIP.
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                                                                                                         MEDLINE=91266957; PubMed=2050149;
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SMART; SM00458; RICIN; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S16022; S16022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562 AA;
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                                                                            SEQUENCE FROM N.A.
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320
                                            NCBI_TaxID=3816;
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360
403
448
487
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34.5%; Score 353.5; DB 1; Length 562;

Query Match

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                                                                                                                                                                          93 SERESIEVGIDVINAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 148
                                                                                                                                                         125
                                                                                                                                                                                                                                                                                   149 DLERWAHQTREBISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYKXI 205
                                                                   65
                                                                                                           92
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-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rnw.
-!- SUBUNIT: DISULFIDE LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELLONGS TO THE RIBOSOME-
-!- SIMILARITY: CONTAINS 2 ricin B-type lectin domains.
                                                                                                    35 ODOVIKFTTEGATSOSYKOPIBALKOKLIGG--LIHDIPVLPDPTTVBERNKYITVELSN
                                                                                                                                                         66 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGNYD
                                                                                                                                                                                                                                               126 RIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFQYI
                                                                6 OYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 3.2.2.21) ADITA-D B CHAIL).
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimura M., Sumizawa T., Funatsu G.;
"The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic proteins from the seeds of Abrus precatorius.";
Biosci. Biotechnol. Biochem. 57:166-169(1993).

!- FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL SYNTHESIS TREOMY ADENINE FROM POSITION 4,324 OF 28 S. RENA. ABRIN-A IS MORE TOXIC THAN RICIN.

-!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBERANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y., "Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.", J. Mol. Biol. 229:263-267(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABRR ABRR STANDARD; PRT; 527 AA.

100077; PR1374;
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
(EC 3.2.2.23); Abrin-b B chain]
                     70; Indels
45.5%; Pred. No. 2.7e-25;
                          24; Mismatches
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MEDLINE=93132798; PubMed=8421313;
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                          Conservative
                                                                                                                                                                                                                                                                                                                                          186 EGEMRTRIR 194
                                                                                                                                                                                                                                                                                                                                                                                   206 SNRVGVSIR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 260-527.
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI
                                                                                                                                                                                        Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Pyrrolidone carboxylic acid.

1 250 ABRIN-B A CHAIN.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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BY SIMILARITY.
PYRROLIDONE CARBOXYLIC ACID (BY
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RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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S -> N (IN REF. 2).
L -> M (IN REF. 2).
Y -> D (IN REF. 2).
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1-GAMMA.
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SMART; SM00458; RICIN, 2.
PROSITE; PS50231; RICIN B LECTIN, 2.
PROSITE; PS00275; SHIGA RICIN; 1.
              PIR; S32430; S32430.
HSSP; PILL40; LABR.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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                                                                                 Pfam; PF00652; Ricin B lectin; 6. Pfam; PF00161; RIP; 1.
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EMBL; M98345; AAA32625.1;
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Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
Biochem. J. 309:285-298(1995).
-!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S TRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRANTHE-MAXIMONIC2; TISSUE=Leaf;
MEDILINE=90256790; PubMed=2141400;
Chow T., Feldman R.A., Lovett M., Piatak M.;
Lisolation and DNA sequence of a gene encoding alpha-trichosanthin, a
"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a
type I ribosome-inactivating protein.";
J. Biol. Chem. 265:8670-8674(1990).
                                                                           01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein alpha-trichosanthin precursor
(rRNA N-glycosidase) (EC 3.2.22) (Alpha-TCS).
Trichosanthes Airllowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliaphyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Tuberous root;
Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
Tian G.Y., Ni C.Z.;
Solentific evaluation of Tian Hua Fen (THF): history, chemistry and
application.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Maximowicz; TISSUE=Tuberous root;
MEDLINE=90256789; PubMed=2341339;
Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
Wu P., Hwang K., Piatak M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin."; J. Biol. Chem. 265:8665-8669(1990).
                                                                                                                                                                                                                                                                                                                 STRAIN=Maximowicz;
MEDILINE=9115367; PubMed=1999291;
Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
"Cloning of trichosanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
"Structure of trichosanthin at 1.88-A resolution.";
Proteins 19:4-13(1994).
                      289 AA
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                   PRT;
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                                                           01-MAR-1989 (Rel. 10, Created)
                   STANDARD;
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PDB; 1J4G; 28-JAN-03.

PDB; 1J5 21-JAN-03.

PDB; 1J0D2; 24-ARR-00.

InterPro; IPR001574; RIP.

PFfam; PF00161; RIP; 1.

PROSITE; PS00275; SHIGARICIN.

PROSITE; PS00275; SHIGARICIN.

PROSITE; PS00275; Antivital; Protein synthesis inhibitor; Hydrolase;
                                                                                         RIBOSOME-INACTIVATING PROTEIN ALPHA-
                                                                                                           | FLL -> LPLI (IN REF. 4).
| MISSING (IN REF. 4).
| -> L (IN REF. 4).
| V -> VDAGLERNAYL (IN REF. 4).
| KI -> GL (IN REF. 4).
| K -> S (IN REF. 4).
| WS -> LWL (IN REF. 4).
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| WS -> LWL (IN REF. 4).
| WS -> T (IN REF. 4).
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| MISSING (IN REF. 2).
                                                                                              TRICHOSANTHIN.
MISSING IN MATURE PROTEIN
BY SIMILARITY.
  or send an email to license@isb-sib.ch).
                                                                                 3D-structure.
           EMBL; M34858; AAA34207.1; -. EMBL; J05434; AAA34206.1; -.
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                                                                                                                                                                                                                                                                                                                            25 VSFRLSGATSSSYGVFISNIRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADB
                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 IISVAIDVINVYIMGYRAGDISYFF---NEASAIEAAKYVFKDAMRKVTLPYSGNYERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoconjugates.";

Bioconj. Chem. 5:423-429(1994).

-i- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at or specific adenosine on the 28S FRMA.

-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                          54; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIP2 BRYDI STANDARD; PRT; 282 AA.
P98184; Q9SBJO;
P616-COT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-FEB-2003 (Rel. 42, Last annotation update)
29-FEB-2003 (Rel. 41, Last annotation update)
glycosidase) (RC 3.2.2.22) (BD2).
Bryonia dioica (Red bryony)
Bryonia dioica (Red bryony)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Siegall C.B., Gawlak S.L., Marquardt H.;
"Bryodin 2 a ribosome-inactivating protein isolated from the plant
Bryonia dioica.";
Patent number USS597569, 28-JAN-1997.
                                                                                                                                                         Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95151812; PubMed=7849072;
Siegall C.B., Gawlak S.L., Chace D., Wolff B.A., Mixan B.,
Marquardt H.;
                                                                                            31676 MW; 5CE09BB630575BB9 CRC64;
                                                                                                                                                         33.4%; Score 342; DB 1;
39.5%; Pred. No. 1.4e-24;
trive 46; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; I34238; -; NOT_ANNOTATED_CDS.
HSSP; P09989; 1MRJ.
                                                                                                                                 Ouery Match
Best Local Similarity 39...
Local Similarity 39...
260 2
263 2
266 2
289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189 MRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 IGKRV 198
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                                                                                                                                                                                                                                                                                                                                                                     69 LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE 128
                                                                                                                                                                                                                                                                                                                                                                                                      81 ESVTVALDVVNVYVVAYRAGNTAYFL---ADASTEANNVLFAGI-NHVRLPYGGNYDGLE 136
                                                                                                                                                                                                                                                                                                                           24 INFSLIGATGATYKTFIRNLRTKLTVGTPRVYDIPVLRNAAAGL---ARFQLVTLTNYNG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPN-RVGLPINQRFILVELSNHAE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                             129 QLAGNL-RENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Root tuber;
MEDLINE=97356562; PubMed=9212998;
Mizukami H., Tida K., Kondo T., Ogihara Y.;
"Cloning and bacterial expression of a gene encoding ribosome-inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60S RIBOSOWAL SUBUNITS. CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                                                                         RIBOSOME-INACTIVATING PROTEIN BRYODIN II
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific adenosine on the 28S rRNA.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC
                                                                                                                                                                                                                                                       13;
                                                                                                                                                          -LINKED (GLCNAC. ..) (POTENTIAL) C52BE2F6A873769C CRC64;
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MEDLINE-92005921; PubMed=1914000;
TYOYOkawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
"The complete amino acid sequence of an abortifacient protein,"
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN.
PLant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; Multigene family; Glycoprotein; Signal.
                                                                                                                                                                                                                    DB 1; Length 282;
                                                                                                                                                                                                                                                       57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribosome-inactivating protein karasurin precursor (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-glycosidase) (BC 3.2.2.22).
Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                                                                                                                    33.3%; Score 341.5; DB 1
48.0%; Pred. No. 1.5e-24;
                                                                                                                                                              N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-1992 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           289 AA
                                                                                                                                                                                                                                                       23; Mismatches
                                                                                                                                             BY SIMILARIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kirilowii var. japonica.";
Biol. Pharm. Bull. 20:711-713(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                       22 282 RI
183 183 BY
25 25 N-
282 AA, 30754 MW;
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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P24478;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 OLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                    25 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHLTNYADE 81
                                                                                                                                                                                                                                                                                                                                                                                             10 INFITAGATVQSYTNFIRAVRGRLTIGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96215449; PubMed=8647092;
Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
"Characterization and molecular cloning of Sambucus nigra agglutinin V
(nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra).";
Eur. J. Biochem. 237:505-513(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P331@3; P33184; P93542; 01-007-1993 (Rel. 27, Created) 01-007-1993 (Rel. 27, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Nigtin b precursor (Agglutinin V) (SNAV) (Contains: Nigrin b A chain CrRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain]. Sambucus nigra (European elder).
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R., Munoz R., Arias F.J., Calonge M., Garcia J.K., Mendez E.; "Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Mol. Biol. 22:1181-1186(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                     PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                       Length 289;
                                                                                                                                                                                                                                                                                                                                                           53; Indels
                                                                                                                                                                                                                                                                 BY SIMILARITY.
883D3E3242887B26 CRC64;
                                                                                                                                                                                                                             KARASURIN-A.
REMOVED IN MATURE FORM.
                                                                                                                                                                                                                                                                                                                       33.0%; Score 338; DB 1; 40.0%; Pred. No. 3.3e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 AA.
                                                                                                                                                                                                                                                                                                                                                           46; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94003077; PubMed=8400135;
                                                                                                                                                                                                                                                                183 183 B'
289 AA; 31704 MW;
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                 EMBL; AB000666; BAA21786.1;
                                                                HSSP; P09989; 1MRJ.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                             21
270
270
289
                                PIR; JC5606; JC5606.
PIR; JU0393; JU0393.
                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 MRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 IGKRV 198
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                                                                                                                                                                          Ioxin; Signal
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SEQUENCE
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142 DNLETAANTRRESIELGPSPLDGAITSLYHGD----SVARSLLVVIQMVSBAARFRY 194
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                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93132798; PubMed=8421313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91201329; PubMed=2016300;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-251 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRECEDES ENDOCYTOSIS.
                                                                                                            STANDARD;
                        185 IEGEMRTRIR 194
                                               195 İBQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 262-528
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-251.
                                                                                                                                                                                                                                             NCBI_TaxID=3816;
                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Seed;
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                                                                                               ABRA_ABRPR
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 NGNTVTLAVDVTNLYVVAFSGNANSYFF-----KDATEVQKSNLFVGTKQN-TLSFTGNY 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                   -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN PARILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 YPSVSFNI.DGAKSATYRDFLSNI.RKTVATGTYEVNGLPVI.RRESEVQVKSRFVLVPI.TNY
                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00275; SHIGA_RICIN; 1.
PROSITE; PS50231; RICIN B_LECTIN; 2.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRNA.
PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROT SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS. THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. B CHAIN IS A CALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       () (POTENTIAL) () (POTENTIAL) () (POTENTIAL) () (POTENTIAL) () (POTENTIAL) ()
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
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F250CBE24621BF14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                            NIGRIN B A CHAIN.
NIGRIN B B CHAIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC..
N-LINKED (GLCNAC...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                  entities requires a license agreement (S. or send an email to license@isb-sib.ch).
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N-LINKED
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InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF001651; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; I.
PRINTS; PR00396; SHIGARICIN.
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les 75; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAWMA).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
-!- SIMILARITY: CONTAIN PARMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                   (EC 3.2.2.2.3) ADILITY B CHALLI.
Abrus precatorius (Indian licore) (Crab's eye).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;
"The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from the seeds of Abrus precatorius.";
Agric. Biol. Chem. 52:1095-1097(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *LAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
**MEDLINE=9533188; PubMed=760890;
Tablirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;
"Crystal structure of abrin-a at 2.14 A.";
J. Mol. Biol. 250:354-367(1995).
-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTRIN
SYNTHESIS TRROUGH THE CATALITIC INACTIVATION OF 60S RIBOSOMAL
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA-ABRIN-A IS MORE TOXIC THAN RICIN.
-!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
Primary structure of three distinct isoabrins determined by cDNA
sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
PIII40; P28589;
01-JUL-1989 (Rel. 11, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-a precursor [Contains: Abrin-a A chain (rRNA N-glycosidase)
(EC 3.2.2.2); Abrin-a B chain]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evensen G., Mathiesen A., Sundan A., "Direct molecular cloning and expression of two distinct abrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92371656; PubMed=1505674;
Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;
"The complete primary structure of abrin-a B chain.";
"RES Lett. 309:115-118(1992).
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70 SVTLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 127
                                                                                                                                                                                                                                                                                                                                     10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                         5 IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLPDPTTLQBRNRYITVELSNSDTE
                                                                                                                                                                                                                                                                                                                32.1%; Score 329.5; DB 1; Length 528; 42.8%; Pred. No. 4.2e-23; Live 28; Mismatches 66; Indels 13;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                              EX SIMILARITY.

INTERCIAIN (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

PYRROLIDONE CARBOXYLIC ACID.

N-LINKED (GLCNAC...).

N-LINKED (GLCNAC...).

M-SSING (IN REF. 4).

M -> Y (IN REF. 4).

M -> L (IN REF. 4).

V -> L (IN REF. 4).
                                                                                                           ABRILLA
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
1-ALPHA.
1-BETA.
2-ALPHA.
2-BETA.
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EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 187
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-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO PRODUCE A SHORTER PROTEIN.
                                                                                                                                                                                                                                                         P313B5; Q9S819;
01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
(RC 3.2.2.22) (BD1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant
                                                                                                                                                                                                                                                                                                                                                                 Bryonia dioica (Red bryony).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Cucurbitales; Cucurbitaceae, Bryonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BIOTECHNOLOGY: Especially useful as immunotoxin for pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97228081; PubMed-9115985;
Gawluk S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.
Siegall C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'N-terminal sequence of some ribosome-inactivating proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
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                                                                                                                                                                                                                                              290 AA.
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MEDLINE=95151812; PubMed=7849072;
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TYPE 1 RIP SUBFAMILY.

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EMBL outstation
                                                                                                     RIBOSOME-INACTIVATING PROTEIN BRYODIN I.
MISSING IN MATURE PROTEIN.
BY SIMILARITY.
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N-LINKED (GLCNAC. .) (POTENTIAL)
E-Xf. REDUCES ACTIVITY:10-FOLD.
RSSIS -> LRHXI (IN REF. 3).
                                                              Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; Slortructure; Multigene family; Glycoprotein; Signal.
1 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                     30.4%; Score 312; DB 1; Length 290
37.3%; Pred. No. 8.6e-22;
tive 46; Mismatches 58; Indels
the Swiss Institute of Bioinformatics and the
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                                        EMBL, 124020; -; NOT ANNOTATED CDS.
PIR; S16491; S16491.
PDB; 1BRY; 04-MAR-98.
INTERPRO; IPRO01574; RIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S2 TISVAVDVINVYIMGYLAGDVSYFF---NEASATEAAKFVFKDAKKKVTLPYSGNYERLQ 138
                                                                                   129 QLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                                                                   70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-:- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
(EC 3.2.2.22).

Luffa cylindrica (Smooth loofah) (Sponge gourd).

Luffa cylindrica (Smooth loofah) (Sponge gourd).

Bukaryots, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            Islam M.R., Hirayama H., Funatsu G., "Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (Luffa cylindrica) seeds.", Agric. Biol. Chem. 55:229-238(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.3%; Score 300.5; DB 1; Length 250; 34.2%; Pred. No. 8.4e-21;
                                                                                                                                                                                                                                               01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F01A8DC8A1078700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEAM; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91248488; PubMed=136866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 AA; 27293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 RTRIRYN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 IERIPKN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; JN0108; JN0108.
HSSP; P16094; 1AHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                     189 MRTRI 193
                                                                                                                                                             194 IGKRV 198
                                                                                                                                                                                                                          RIPB LUFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACT SITE
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                                                                                                                                                                                                              RIPB_LUFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                  RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 NTITMAVDVTNVYIMGYLVNGTSYFF---NETDAQLASKFVFQGTKSITLPYSGNYQKLQ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 QLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARPQYIEGE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Biotechnol. 17:337-340 (2000).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRMA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 INFTIAGATVOSYTNFIRAVRGRLTTGADVRHEIPVL-PNRVGLPINQRFILVELSNHAE
                                                                                   16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae, Cucumis.
NCBI_TaxID=131071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00161; RIP; 1.
RNUTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.9%; Score 296.5; DB 1; Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                            Yamada T., Ohki S.T., Osaki T.;
"Cloning and analysis of a cDNA coding a putative ribosome-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 POTENTIAL.
286 FUTATIVE RIDOSOME-INACTIVA
1185 N-LINKED (GLCNAC. .) (PO
110 N-LINKED (GLCNAC. .) (PO
252 N-LINKED (GLCNAC. .) (PO
31771 MW; 4EFD4966E604DA41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inactivating protein from Cucumis figarei.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB045560; BAB19677.1; -.
HSSP; P16094; IAHC.
InterPro; IPR001574; RIP.
                                                       16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.4%;
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 MRTRIRYNR 197
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196 IIDRISVSK 204
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252
286 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                         Cucumis figarei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxin; Signal
CUCFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT SITE
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FEBS Lett. 399:153-157(1996).

-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN

SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL

SYNTHESIS THROUGH THE CATALYTIC INACTIVATION 6, 224 OF 28 SRNA. THE

B CHAIN BINDS TO CELL RECEPTORS AND PROBBLY FACILITATES THE ENTRY

INTO THE CELL OF THE A CHAIN; B CHAIN'S ARE ALSO RESPONSIBLE FOR

CELL AGGLUTINATION (LECTIN ACTIVITY).

-! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one

specific adenosine on the 268 rRNA.

-! SUBUNIT: Disulfide-linked dimer of A and B chains.

-! SUBUNIT: Disulfide-linked dimer of A and B chains.

-! STAMMACEUTICAL: Due to its immunomulative effects it is being

studied in clinical trials in cancer patients as it may slow the

growth of cancer cells and be an effective treatment for solid
                                                                                                                                                                                                                                                                                     "Complete amino acid sequence of the A chain of mistletoe lectin I."; FEBS Lett. 399:153-157(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND NON-GIYCOSYLATED FORM MLA'.
SIMILIARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA
                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Santalales; Santalaceae; Viscum.
                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2013 (Rel. 41, Last amnotation update)
glycosidase) (EG 3.2.2.22).
Viscum album (European mistletoe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant defense; Hydrolase; Toxin; Repeat; Glycoprotein; Lectin. ACT_SITE 165 165 BY SIMILARITY.
                                                                                                                                                                                                                                              MEDLINE=97134581; PubMed=8980141;
Soler M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.9%; Score 286; DB 1; Length 254; 38.4%; Pred. No. 1.9e-19; ive 36; Mismatches 56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IN MLA').
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> Y (IN MLA').
-> A (IN MLA').
-> D (IN MLA').
-> B (IN MLA').
-> F (IN MLA').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PP -> ST (IN MLA')
T -> S (IN MLA')
D -> S (IN MLA')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N -> T (IN MLA')
P -> T (IN MLA')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E -> D (IN MLA')
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T -> S (IN MLA')
 254 AA.
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 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001574; RIP.
STANDARD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00161; RIP;
                                                                                                                                                                                                                                STRAIN=Subsp. album;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P11140; 1ABR.
                                                                                                                                                                                                                                                                               Voelter W.;
 VISAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 129
69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDILINE=92288316; PubMed=1600156; Maeuta C., Koiwai A.; Katacka J., Habuka N., Miyano M., Maeuta C., Koiwai A.; Katacka J., Habuka N., Miyano M., Maeuta C., Koiwai A.; Mucleotide Sequence of CDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffa cylindrica."; Plant Mol. Biol. 18:1199-1202(1992).

-! - CAPALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.

-! SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 VRFSLSGSSSTSYSKFİGDLRKALPSNGTVYNITLLLSSASGA---SRYTLMTLSNYDGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1992 (Rel. 24, Last sequence update)
28-FFB-2003 (Rel. 41, Last annotation update)
28-FFB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-alpha precursor (rRNA
N-glycosidase) (RC 3.2.2.22)
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota; Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIBOSOME-INACTIVATING PROTEIN LUFFIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
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                                                                                                 132 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARF-
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                                                                                                                                                                                                                                                                                                     179 YINSGASFLPDVYMLELETSWGQQSTQVQHS 209
                                                                                                                                                                                                                                         ----GEMRTRIRYN 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last seqn
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X62371; CAA44229.1; -. PIR; S22494; S22494.
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InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO
TYPE 1 RIP SUBFAMILY.
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                                                                                                                                                                                                                               184 YIE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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72 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 131

14 TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV 9 THQTTGEEYPRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGQDSV

Conservative

Similarity 81;

Local

Matches

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                               130 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ortigao M., Better M.;
"Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologome inactivating proteins.";
Nucleic Acids Res. 20:4662-4662[1992].
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific achenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
Ribosome-inactivating protein momoration in precursor (rRNA N-glycosidase) (EC 3.2.2.2)
N-glycosidase) (EC 3.2.2.2)
Nomoratica balsamine (Bitter gound) (Balsam pear).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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PIR; S25560; S25560.
PDB; JCF; 07-JUN-9DB; 07
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35.3%; Pred. No. 9.9e-19;
... Mismatches 67; Indels 12; Gaps
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NCBI_TaxID=3672;
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BY SIMILARITY
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                                                                                                                                 190 RTRIRYNR 197
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P29339;
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Listing first 45 summaries
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2: sp_bacteria:*
3: sp_fungi:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                    SPTREMBL 23:*
                                                                                                                                                                                                                  BLOSUM62
                                                                                                                                                                     1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110:
                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                Scoring table:
                                                             OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                     Sequence:
                                                                                            Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q41174 ricinus com	Q94bw3 cinnamomum	Q94bw4 cinnamomum	Q94bw5 cinnamomum	Q9fv22 cinnamomum	004367 sambucus ni	Q9avr2 sambucus eb	10	Q94ke4 trichosanth	Q9lre3 trichosanth	Q41216 trichosanth	Q38760 abrus preca	Q945s2 sambucus ni	Q8gt32 sambucus ni	Q38761 abrus preca	Q8lpv7 trichosanth
ID	041174	Q94BW3	Q94BW4	Q94BW5	Q9FV22	004367	Q9AVR2	206076	Q94KE4	Q9LRE3	041216	Q38760	Q945S2	Q8GT32	038761	Q8LPV7
DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
% Query Aatch Length DB	541	580	580	581	549	563	564	528	289	247	289	252	563	563	252	270
% Query Match	99.2	39.2	38.8	38.8	38.6	34.2	33.9	33.6	33.2	33.0	33.0	32.8	32.2	32.2	32.1	31.6
Score	1017	401.5	397.5	397.5	395.5	350.5	347.5	344.5	340	338	338	336.5	330.5	330.5	329.5	324
Result No.	 	2	e	4	5	9	7	c o	σ	10	11	12	13	14	15	16

	01 O M 10 10 :		3 viscu 7 momor 8 sambu 6 viscu 7 viscu 7 momor	004358 iris hollan QQWX27 iris hollan 004356 iris hollan Q9m653 polygonatum Q8gzn9 euphorbia s Q8wyu0 jatropha cu Q8w2e8 iris hollan
Q96236 Q96237 Q04071 Q91611 Q96235	004072 Q00980 Q41358 Q8LKQ5 O22415	Q9M654 Q8LKQ4 Q8LKQ6 Q9FSH2 Q8S452	Q8W243 Q9FUV7 P93543 Q8RXH6 Q8RXH7	004358 Q8W2E7 004356 Q9M653 Q8GZN9 Q8VYU0
00000	1000	10000	22222	110000
251 251 565 270 251	566 278 570 249 570	604 251 251 264 293	565 586 531 249 286	298 300 300 603 299 293
31.6 31.5 31.1 30.9 30.9		27. 27. 27.	27. 27. 26.	266.5 266.3 255.0 255.6 255.6
323.5 322.5 319 317 316.5	310.5 307.5 291 285 285	283.5 283 282 280 278	277.5 277 277 275 273 273	272 270 268 266.5 262.5 261 259
11 118 119 22 22	22 2 2 2 2 4 4 2 4 4 4 4 4 4 4 4 4 4 4	28 30 31 32	######################################	W 4 4 4 4 4 4 W 0 11 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13

ALIGNMENTS

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RESULT 1

Q41174 PRELIMINARY; PRT; 541 AA.

AC Q41174;
D q41174 PRELIMINARY; PRT; 541 AA.

AC Q41174;
DT 01-NOV-1996 (TYEMBLTE1. 01, Created)
DT 01-NOV-1996 (TYEMBLTE1. 01, Last sequence update)
DT 01-NOV-1996 (TYEMBLTE1. 23, Last annotation update)
DT 01-NOV-1996 (TYEMBLTE1. 23, Last annotation update)
DT 01-NAR-2003 (TYEMBLTE1. 23, Last annotation update)
DE PROTICID A Canain (EC 3.2.2.22) (TRNA N-glycosidase)
DE PROTICID A Canain (EC 3.2.2.22) (TRNA N-glycosidase)
OC Eukaryota, Viridiplantae; Sirreptophyta; Embryophyta; Tracheophyta;
C Eukaryota, Viridiplantae; Sirreptophyta; Embryophyta; Tracheophyta;
C Eukaryota, Viridiplantae; Sirreptophyta; Embryophyta; Core eudicots; Rosidae;
CC Eukaryota, Viridiplantae; Buphorbiaceae; Ricinus.

NOSI TARIDIANE-92338377; PubMed=1633311;
RX MEDLINE-92338377; PROMING THE 288 RRNA.
C -: CATALITY AND THE 288 RRNA.
C -: STMILLARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
DR RISSP; PO2879; BRG.
DR RESPEROSES; RICIN B.
DR RINGSP; PO2879; BRG.
DR REATH PROMISSY; RICIN B. LECTIN; C.
DR REATH PROMISSY; RICIN B. LECTIN; C.
DR ROSITE; PS00318; RICIN; 1.
DR ROSITE; PS00318; RICIN; 2.
DR ROSITE; PS00318; RICIN; 2.
DR ROSITE; PS00318; RICIN; 2.
SEQUENCE 541 AA; 60281 MM; 2B7B2CDEFIF2E9D9 CRC64;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q94BW5;
                                                                                                                         Q94BW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STONAL
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                                                                                                              094BW4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
                                                                                  RESULT 3
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ID Q9
AC Q9
DT 01
DT 01
DE TY
DE (F
                                                                                               094BW4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 AADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 DLERVAGERREEILLGMDPLENAISALMISNL--NQQRALARSLIVVIQMYAEAVRFRFI 206
                                                                                                                                                                  181
                                                                                                                                                                                            121 GNYDRLEOLAGNIRENIELGNGPLEEAISALYYSTGGTQLPTLARSFIICIOMISEAAR 180
                                                                                                              ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                      ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Yang O., Gong Z.Z., Liu W.Y.; Yang O., Gong Z.Z., Liu W.Y.; "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI
                                                                        7 YPIINFITAGAIVQSYINFIRAVRGRLITGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                         2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                  GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AV03903; AAK82460.1, --
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00552; Ricin_B_lectin; 6.
Pfam; PF00652; Ricin_B_lectin; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
NCBI_TaxID=13429,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 580 TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.
580 AA, 64421 MW, 940D10F01E7FB558 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                    Type 2 ribosome-inactivating protein cinnamomin III precursor (EC 3.2.2.22) (rRNA N-glycosidase).
Cinnamomum camphora (Camphor tree).
Score 1017; DB 10; Length 541;
Pred. No. 1.9e-87;
1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.2%; Score 401.5; DB 10; Length 50.0%; Pred. No. 2.8e-29; tive 28; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS, PR00396, SHIGARICIN.
SMART, SM00458; RICIN; 2.
PROSITE, PS50231; RICIN B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                       FOYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                                                                                 181 FOYIEGEMRTRIRYNRRS 198
  99.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                              Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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66 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patterns.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 YQTVTFTTKNATKTSYTQFIEALRAQLASGEE-PHGIPVMRDGSTVPDSKRFILVELSNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AY039802; AAK82459.1; -.
                                                                                                                                                                                                                                                                                                                                                                   Type 2 ribosome-inactivating protein cinnamomin II precursor (EC 3.2.2.2.2) (FRMA N-glycosidase).
Cinnamomum camphora (Camphor tree).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of three type 2 RIP (ribosome-inactivating progenes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%; Score 397.5; DB 10; Length 580; 49.5%; Pred. No. 6.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Last Sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin I precursor
(EC 3.2.2.2) (FRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CINNAMOMIN II.
37E4289ECCE0CBFF CRC64;
                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PR00396, SHIGARICIN.
SMART, SMORSE, RICIN, 2.
PROSITE, PS5021, RICIN B.LECTIN; 2.
Hydrolase, Signal, Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro, IPR000772; Ricin_B_lectin.
Interpro, IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00652; Ricin B lectin;
Pfam; PF00161; RIP; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 AA; 64265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu W.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 EYRVRESI 214
186 EGEMRTRI 193
                                                       207 EYRVRESI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Yang Q., Gong Z.Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFOYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33 YQTVTFTTKNATKTSYTQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xie L., Liu W.-Y., Wang E.-D.;
"Molecular cloning of cinnamomin A-, B-chain and the expression,
"Molecular cloning of cinnamomin A-, B-chain and the A-Chain.";
Submitfication, characterization and mutagenesis of the A-Chain.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: EMDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF259548; AAF68978.2; --
                                                                                                                                                                            Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                         "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.8%; Score 397.5; DB 10; Length 581;
50.0%; Pred. No. 6.7e-29;
iive 27; Mismatches 60; Indels 7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ©9FV22;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last amnotation update)
Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.2) (rRNA
                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Introduction (Interpretation of Camphor tree).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lauraceae; Cinnamomum.
Cinnamomum camphora (Camphor tree).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magmoliophyta, Laurales, Lauraceae, Cinnamomum.
NCBL_TaxID=13429,
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CINNAMOMIN I.
6E8F5FB8FBA3D196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 AA.
                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                             PROSITE, PS50231; RICIN B LECTIN; 2. Hydrolase, Signal, Toxin.
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                                                                                   SEQUENCE FROM N.A. Yang Q., Gong Z.Z., Liu W.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581 AA; 64215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-glycosidase) (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=13429;
                                                                                                                                                               patterns.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 AADSPVTLAVDVTWAYVVAYRTGSQSFFLREDNP--PAIENLLPDTK-RYTFPFSGSYT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; plant J. 12,225-1266(1997).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARYTY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. HSSP; PO2879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                             38.6%; Score 395.5; DB 10; Length 549; 50.0%; Pred. No. 9.5e-29; tive 27; Mismatches 60; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-UUL-1997 (TrEMBLrel. 22, Last annotation update)
Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA N-glycosidase)
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Peumans W.J.;
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549 AA; 60648 MW; 02607FE607CA44B0 CRC64;
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InterPro; IPR001574; RIP.
Pfam; PF0055; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                           PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS50231, RICIN B LECTIN, 2.
PROSITE, PS00275, SHIGA RICIN, 1.
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                                                                Pfam; PF00652; Ricin B lectin; 5.
Pfam; PF00161; RIP; 1.
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SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                           94; Conservative
                                          InterPro; IPR001574; RIP.
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SIGNAL 1 25
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563 AA;
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SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Created)
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InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
PRIMTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
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HSSP; P11140; 1ABR.
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                                                                                        185 IEGEMRTRIR 194
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195 IEQEVRRSLQ 204
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528 AA;
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Best Local
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-- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
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                                                                                            7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH
                                                                                                                                       28 YPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFVLVLLTNY
                                                                                                                                                                                     67 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI -- THLFIDVQNRYIFAFGGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                               15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIFIC ADBROSINE ON THE 288 RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AJ40822; CAC33178.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sambucus ebulus.
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
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       DB 10; Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56; Indels
                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EBULIN L A-CHAIN.
EBULIN L B-CHAIN.
8261681A6DB55CB8 CRC64;
  Query Match
34.2%; Score 350.5; DB 10;
Best Local Similarity 41.6%; Pred. No. 1.8e-24;
Matches 79; Conservative 40; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.4e-24;
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41.1%; Pred. No. 3.4e-
tive 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50231; RICIN B LECTIN; 2. PROSITE; PS00275; SHIGA RICIN; 1. Glycosidase; Hydrolase; Signal; Toxin. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P02879; 2AAI.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; I_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     185 IEGEMRTRIR 194
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-! CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 288 RRNA.

-! SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
01-NOV.1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Abrin-d (EC 3.2.2.2) (rRNA N-glycosidase) (Fragment).
Abrin-precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58870 MW; 62ED42FB8FFE60F8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 SVTLALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
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-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AB039324; BAA92530.1; --
HSSP; P09989; 1MRJ.
                                                                                                                                                                                                                                                                            Yuan H., Wang L., Wang Y., An C., Chen Z.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trichosanthes sp. Bac Kan 8-98.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Gaps
                                                                                                                                                                                                                                                                                                                                                    SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF367252; AAK52960.1; -.
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"Genomic DNA Clone for mature typ-1 ribosome-inactivating protein
Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
                       01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase)
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24 270 TRICHOSANTHIN.
289 AA; 31706 MW; A6D5602549CAS657 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.2%; Score 340; DB 10; 39.5%; Pred. No. 6.8e-24;
                                                                                                  Trichosanthes kirilowii (Mongolian snake-gourd)
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PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Signal; Toxin.
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Best Local Similarity
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCBI TaxID=3677;
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Q9LRE3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 128
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Zheng H., Wang B., Shaw P., Yeung H.;
Zheng H., Wang B., Shaw P., Yeung H.;
[Cloning and DNA sequencing of the gene encoding trichosanthin].";
I Chuan Haush Pao 21:42-51(1994).
-! - CATALYTIC ATTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-! SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 IISVAIDVTNVYVMGYRAGDISYFF---NEASAIBAAKYVFKDAKRKVTLPYSGNYERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                2 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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                                                                                                                                                                                                                                                                                                                                                  10 INFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                              33.0%; Score 338; DB 10; Length 247;
40.0%; Pred. No. 9.5e-24;
tive 46; Mismatches 53; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 289;
                                                                                                                                                                       247 AA; 27199 MW; 89811AC32892F03F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 AA; 31650 MW; 286AC14D48BCA175 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichosanthin (EC 3.2.2.22) (FRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 33.0%; Score 338; DB 10; Best Local Similarity 39.5%; Pred. No. 1.1e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                           PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                        74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S70176; AAB31048.1;
HSSP; P09989; 1MRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                               247
Pfam; PF00161; RIP; 1
                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189 MRTRI 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 171 IGKRV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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177 GVSIR 181
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Q945S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 WAHQTREQISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYISNRV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 129
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       129 OLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 188
                                                 6 IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLRDPTTVEERNRYITVELSNSERE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
NCBI_TaxID=3816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIFIC ADENOSINE ON THE 28S RRNA.

-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS. BACH DOMAIN
CONSIGNS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 266:6848-6852(1991).

-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S.RNA.ABRINT A IS MORE TOXIC THAN RICIN.

-!- FUNCTION: THE B CHAIN IS A GALACIOSE-SPECIFIC LECTIN THAT FACILITARES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evensen G., Mathiesen A., Sundan A.;
"Direct molecular cloning and expression of two distinct abrin A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٠,
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Glycogidase; Toxin; Repeat; Glycoprotein; Lectin.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Abrus precatorius (Indian licorice) (Crab's eye)
                                                                                                                                                                                                                                                                                                                                                                                                   252 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS. BELONGS TO TYPE 2 RIP.
EMBL; X54872; CAA38654.1; -.
HSSP; P11140; 1ABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91201329; PubMed=2016300;
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Pfam; PF00161; RIP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                189 MRTRI 193
                                                                                                                                                                                                                    194 IGKRV 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=LEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             038760;
                                                                                                                                                                                                                                                                                                                                                                                                   038760
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                                                                                                                                                                                                                                                                                                                               RESULT 12
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67 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI -- THLFTDVQNRYTFAFGGNY 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF409135; AAL04123.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Damme E.J.M.; "Characterization and cloning of lectins and ribosome-inactivating proteins from Sambucus nigra leaves.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein nigrin 1 precursor
(EC 3.2.2.22).
Sambucus nigra (European elder).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                     Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Espermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
NCBI_TaxID=4202;
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SEQUENCE 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;
                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein (EC 3.2.2.2) (TRNA
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   563 AA.
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InterPro; IPR001574; Ricin_B lectin.
Fian, PF00652; Ricin_B lectin; 6.
Pfan, PF00161; RIP; I.
PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
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PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                               N-glycosidase)
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124
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                                                                                                        Girbes T., Arias F.J., Antolin P., "Characterization and molecular cloning of Nigrin 1, a type two "Characterization and molecular cloning of Nigrin 1, a type two ribosome-inactivating protein from leaves of elder (Sambucus nigra)."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF249280; AAN86130.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        derived by site-specific mutagenesis in Escherichia coli.";
Eur. J. Biochem. 219:83-87(1994).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                7 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papliionoideae; Abreae; Abrus.
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                                                                                                                                                                                                                                                            DB 10; Length 563;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                        ch 32.2%; Score 330.5; DB 10; Length Similarity 39.5%; Pred. No. 1.4e-22; 75; Conservative 39; Mismatches 61; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ricin A-chain type 73 (EC 3.2.2.22) (FRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evensen G., Mathiesen A., Sundan A.;
Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
                     Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                     Hydrolase, Glycosidase.
SEQUENCE 563 AA; 62173 MW; 0EB236421FC5E04F CRC64;
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PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                      NCBI_TaxID=4202;
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70 SVTLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 127
                                                                                                                                                                                                                                                            64 SIEVGIDVINAYVVAYRAĞIQSYFLRDAÞSSASD----YLFTGT-DQHSLPFYGTYĞDL 117
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                                                                                                                                                                                6 IKFSTEGATSOSYKQFIEALRERLRGG--LIHDIPVLPDPTTLQERNRYITVELSNSDTE 63
                                                                                                                                                     10 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 69
                                                                                                                 13; Gaps
                                                                           DB 10; Length 252;
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                  252 252
252 AA; 28229 MW; 187B6B4E134AECE5 CRC64;
                                                                       / Match 32.1%; Score 329.5; DB 10
Local Similarity 42.8%; Pred. No. 5.5e-23;
hes 80; Conservative 28; Mismatches 66;
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Glycosidase; Hydrolase; Toxin.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Describtion	Ricin A chain. Un	Ricin A-chain (RTA	Ricin A-chain ribo	Ricin A-chain RIP.	Ricin A. Escheric	Sequence of Ricinu	Ricin A encoded by	Anti-cataract immu	Ricin D. Ricinus
		10	AAR37290	AAR63902	AAW25136	AAW21699	AAP70097	AAP70838	AAP95639	AAR70827	94000da
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AAP50166 2 AAG78300 2 AAG78304 AAP70326 8 AAW25787	04004	AAPB0164 4 AAR39571 AAP60240 AAP70325 0 AAP94793 3 AAR30722	4.04.00 0.0	14688466458
565 6 565 22 565 22 576 8 576 18	B 8 8 8 8	9468448	332 11 14 16 17 17 17 17 17 17 17 17 17 17 17 17 17	744446 74446 74446 7446 7446 7446 7446
0.70 0.70 0.70 0.70 0.70	9.79 9.79 9.79 7.79	2 4 4 2 0 0 0 0	999996.98888.5.287.7.2.88	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
			940 934 918 861.5 861.5 801.5 718	
10 11 13 14	11 11 11 11 11 11 11	0	222 233 332 44	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8

ALIGNMENTS

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Type II ribosome-inactivating protein; type II RIP; gelonin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll SF, Lane JA,
                                                                                    AAR37290 standard; protein; 267 AA
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92US-0901707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92WO-US09487.
                                                                                                                                                                                                                                                              (updated)
(updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-167617/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ricin A chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9309130-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-NOV-1991;
                                                                                                                                                                                                                                                         25-MAR-2003
09-JAN-2003
13-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAY-1993.
                                                                                                                                                                         AAR37290;
RESULT 1
                                                                                                                                   X X X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B
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                                                                                                                                                                                                                                                                                                                                             61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                    GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNKVGLPINQRFILV 60
                                                             The invention covers analogues of Type I RIPs. Ricin is a Type II RIP whose A chain is homologous to plant type I RIPs. The analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment.

(Updated on 09-JNM-2003 to correct PN field.)
                                                                                                                                                                                                                                                                           --VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                      10; Gaps
            cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide(s) encoding type I ribosome-inactivating proteins
Analogues of type I ribosome inactivating protein - useful as
                                                                                                                                                                                                                              97.9%; Score 951; DB 14; Length 267; 94.9%; Pred. No. 1.3e-93; ive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricin A chain; RTA; ribosome-inactivating proteins; RIPs; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carroll SF;
                                                                                                                                                                                                                                                                            2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Studnicka GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR63902 standard; protein; 267 AA
                                             Claim 1; Page 92; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   FQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                        181 POYTEGEMRTRIRYNRRS 198
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           graft-versus-host disease.
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carroll SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-006804/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricin A-chain (RTA)
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (XOMA ) XOMA CORP.
                                                                                                                                                                                                        267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricinus communis.
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27-JUL-1995
                                                                                                                                                                                                                                                  Matches 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR63902;
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                                                                                                                                                                                                                                                                                                                                                                     112
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                               Query Match
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111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize, proRIP, ribosome inactivating protein; alpha; beta subunit; internal linker; Barley Translation Inhibitor; Trichosanthin; Ricin A-chain; Abrin-A A-chain; Saporin; SIT-1; Luffin A; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30; therapeutic toxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEI PVLPNRVGLPINORFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Gaps
                                                                                                                                                                                               Which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host
                                                                                                                                             AAR63902 is the ricin A chain gene product, it is analogous to the ribosome-inactivating proteins (RIPs) described in AAR63903-R63911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricin A-chain ribosome inhibitory protein inactive precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
which are suitable for use as components of cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 951; DB 16;
Pred. No. 1.3e-93;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
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                                                                                        Example 3; Fig 1; 221pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 FOYIEGEMRIRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (updated)
                                  therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-JUN-1995;
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07-JUN-1995;
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(DOWC) DOWELANCO.

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/note= "Position of possible insertion of internal
peptide linker sequence"
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                                                                                                                                                                                                                                                                                                                                                      Claim 2; Column 91-94; 121pp; English.
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                                                                                                                                                                                                                               Walsh TA;
                                                                                                                                                   90US-0535636.
                                                                                                          95US-0378761.
                                                                                                                                      92US-0987927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 94.99
                                                                                                                                                                                                                               Hey TD, Morgan AER,
                                                                                                                                                                                                                                                            WPI; 1997-309831/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 290 AA;
                                                                                                                                                                                                (DOWC ) DOWELANCO.
                                                                                                          26-JAN-1995;
                                                                                                                                                   11-JUN-1990;
26-JAN-1995;
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                                              US5635384-A
                                                                           03-JUN-1997
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   BXHXYX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                             AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
which was engineered to contain a selectively removable internal peptide
linker sequence separating the alpha and beta units of the RIP. When
separated the two units regain and test and is of the RIP. When
separated the two units regain and beta units of the RIP. When
cukaryotic ribosomes and hence preventing protein production. Many
different RIPs may be produced with an internal linker including
maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
Saporin. The RIPs can be used in the construction of therapeutic
toxins targeted to specific cells such as tumour cells via the
tatachment of a targeting polypeptide, e.g. a monoclonal antibody.
A further use is in HIV therapy (see U54869903). There is interest
in expressing RIP recombinantly in host eukaryotic cells, because of
the capacity to provide correct post-translational processing. However,
RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
in cell death. Since the inactive RIP proteins are not cytotoxic to
cukaryotic cells, they can be recombinantly expressed in such cells and
then converted to active RIP proteins.
(Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEALTHLFTDVQNRYTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 GNYDRLEQLAGNIRENIELGNGPLERAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNYDRIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- VLPNRVGLPINQRFILV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; linactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidaes; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                        DNA encoding pro-ribosome inactivating proteins - inactive precursors of ribosome inactivating proteins; can be expressed in eukaryotic cells without causing cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.9%; Score 951; DB 18; Length 290; 94.9%; Pred. No. 1.4e-93; ive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT--
                                                                                                                                  Claim 4; Column 91-94; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW21699 standard; Protein; 290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 FQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    205 FOYIEGEMRIRIRYNRKS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                           WPI; 1997-362934/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricin A-chain RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
26-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW21699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
                 Hey TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loca
Matches
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The sequences given in AAW21698-710 represent Ribosome Inactivating Proteins (RIP's), which may be used in the construction of the proteins possible invention. The proRIP has a selectively removable, internal peptide linker. The procursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidaes activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 285 RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive proteins make it possible to provide protein possible. The RIP can be used to make cytotoxic conjugates.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 BLSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VLPNRVGLPINQRFILV 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Gaps
Inactive precursor of maize ribosome-inactivating protein - e
chimeric ribosome-inactivating protein precursors containing
internal linker sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.9%; Score 951; DB 18; Length 290; 94.9%; Pred. No. 1.4e-93; ive 0; Mismatches 0; Indels 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 IFPKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                      97.9%; Score 951; DB 8; Length 332;
94.9%; Pred. No. 1.7e-93;
iive 0; Mismatches 0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of Ricinus communis castor beans ricin toxin (RT or ricin) A protein encoded by pRA123.
                                                                                                                                                                                                                                                             N-terminal methionine free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase
                                                                                                                                                                                                                                                                                                                         Ricin A may be produced in a form which lacks an N-terminal Metusing Met-aminopeptidase from E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                                                                                                   Chang SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP70838 standard; protein; 332 AA.
                                                                                                                                                                                                   Chang S,
                                                                                                                                                                                                                                                                                                    Disclosure; Fig. 4; 20pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOYIEGEMRTRIRYNRRS 233
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/note="Leader"
                                                                                                                                   86US-0860330.
85US-0778414.
                                                                                                           86EP-0307242.
          Ricin A; Met-aminopeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.9<sup>5</sup>
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.,302
                                                                                                                                                                                                   Benbassat A, Bauer KA,
                                                                                                                                                                                                                         WPI; 1987-110172/16.
N-PSDB; AAN70152.
                                                                                                                                                                         (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricinus communis.
                                  Escherichia coli.
                                                                                                                                    06-MAY-1986;
20-SEP-1985;
                                                                                                           19-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
18-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plant toxin.
                                                                                   22-APR-1987
                                                           EP219237-A.
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                                                                                                                                                                                                                                                                                                                                                                   Sequence
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The full-length sequences encoding ricin A (AAN70520), ricin D (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obten using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three plasmids contg. CDNA inserts obtain a CDNA library for sequences encoding ricin B using the probe in AAN70517. The CDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a Hindlif site at the beginning of the mature protein (see AAN70518). The coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression (vectors contg. the PhoA promoter-operator and leader sequence (AAN70523) and sultable retroregulators.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 GNYDRIBQIAGNIRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

97 9%; Score 951; DB 8; Length 332;
Best Local Similarity 94.9%; Pred. No. 1.7e-93;
Matches 188; Conservative 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP95639 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Fig 1; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 FQYIEGEMRTRIRYNRRS 233
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                 315..332
/note="B-chain"
/note="A-chain"
                                                                                                                                                86EP-0308877
                                                                                                                                                                                   86US-0837583
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(updated)
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N-PSDB; AAN70519.
                                                                                                                                                                                                                                           CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 AA;
                                                                                                                                                                                                                       (CETU ) CETUS CORP
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31-OCT-2002
                                                                                                                                                13-NOV-1986;
                                                                                                                                                                                     07-MAR-1986;
                                                                                                           23-SEP-1987
                                                                         EP237676-A.
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                                                                                                                                                                                                                                                                               Piatak M;
                       Region
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                              Recombinant vectors expressing ricin chains or diphtheria toxin -used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain. Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                                                                                      prodn. of new immunotoxin conjugates with monoclonal antibodies, having high cell specificity and good extracellular stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                       Greenfield L, Nitecki D, Kaplan D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.9%; Score 951; DB 10; Length 332; 94.9%; Pred. No. 1.7e-93; rive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                    Plasmid pRA123; ricin-A; ricin-B; cytotoxicity
                 Ricin A encoded by insert from plasmid pRA123.
                                                                                          ..35
label= leader sequence
                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 14; 54pp; English.
                                                                                                                                                                                                                                                                                                         Gelfand D, Lawyer FC, Horn G,
                                                                                                                                                        /label=B-chain
                                                                                                                     /label=A-chain
                                                                                                                            303..314
/label=linker
                                                                                                                                                                                                                                84US-0578115.
84US-0578121.
84US-0578122.
84US-0648759.
84US-0653515.
                                                                                                                                                                                                               89EP-0201162.
                                                                                                                                                                                                                                                                                      CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 94.9
nes 188; Conservative
13-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                   WPI; 1989-286959/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 AA;
                                                      Ricinus communis.
                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN91281
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08-FEB-1984;
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                                                                                                                                                                                                                                                            07-SEP-1984;
20-SEP-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          host cells.
                                                                                                                                                                                             04-0CT-1989
                                                                                                                                                                          EP335476-A
                                                                                                                                                                                                                                                                                                                   Piatak MJ;
                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                        Peptide
                                                                                                           Peptide
                                                                                                                            Peptide
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The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A and a hexa-histatidine tag. The DNA construct encoding the immunotoxin was expressed from pHB19 in E. Coli. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                             Immunotoxin; heavy chain; light chain; variable region; antibody;
ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
pHB19; 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 97.9%; Score 951; DB 16; Length 554; Best Local Similarity 94.9%; Pred. No. 3.4e-93; Matches 188; Conservative 0; Mismatches 0; Indele 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "MAb 4197X heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "phoA signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= LIGHT
/note= "MAb 419X light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549..554
/label= TAG
/note= "hexa-histidine tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wallace TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...27
/label= Sig_peptide
                                                                                                                                                     AAR70827 standard; Protein; 554 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig.4; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= RICIN-A
172 FOYIEGEMRIRIRYNRRS 189
                       216 FQXIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28..145
/label= HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93US-0101329.
                                                                                                                                                                                                                                             (updated)
(first entry)
                                                                                                                                                                                                                                                                                                           Anti-cataract immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gould RM, Kelleher PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-082036/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ85386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9503828-A1
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                                                                                                                                                                                                                                             25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
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112
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                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                         RESULT 10
AAP50166
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                                                                                          à
                                                                                                       112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                       398 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 457
                                                  52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                    278 IFPKQYPIINFTTAGAIVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 337
                                                                            338 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFG 397
21
------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                Ricin D; Ricinus communis; caster beans; Zanibariensis variety; modified; lectin binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B chain is removed or diminished to reduce cell binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 951; DB 10;
Pred. No. 3.5e-93;
0; Mismatches 0;
  2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                              AAP90079 standard; protein; 562 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; fig 1; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                            Ricinus communis (caster beans)
                                                                                                                                                                                172 FQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.9%;
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                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brown EL, Jones S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAN90068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-NOV-1987;
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                                                                                                                                                                                                                                                                                                                 25-MAR-2003
01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1989
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52 ELSNHAELSVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111

36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95

q à

à

IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLT--

Matches 188; Conservative

Local Similarity

51

Gaps

10;

Indels

---VLPNRVGLPINQRFILV

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96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                        GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preproricin is the whole polypeptide encoded by AAN50202 and the DNA encoding this is claimed. Proricin is obtained from preproricin by removal of the AA leader sequence. The linker AA sequence which is present in the precursor polypeptide is enzymatically removed in the cell to separate the A and B chains, which are joined by a disulphide bridge during the formation of the ricin molecule itself. This linker region as well as the presumptive amino terminal leader or signal sequence are not present in the sequences already published by Funatsu et al.
                                                                                                                                                                                                                                                                                                                                                                                                 292..303
/label= links the C-terminus of the A chain and
the N-terminus of the B chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA sequences coding for ricin type plant toxin - mutants, and modified vectors and host microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260..262
/label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398..400
/label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= N-linked glycosylation
                                                                                                                                                                                                                                                                   Sequence of preproricin encoded by pRCL617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 30-30c; 40pp; English
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                       Ą.
                                                                                                                                                                                       AAP50166 standard; Protein; 565
                                                                                            172 FOYIEGEMRIRIRYNRRS 189
                                                                                                                216 FOYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                           /label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84GB-0006569.
83GB-0019265.
83CH-0019265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84EP-0304801
                                                                                                                                                                                                                                                                                             Toxin; anti-tumour therapy
                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438..440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYWA-) UNIV WARWICK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JUL-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1985
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Cleavage-site
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                                                                                                                                                                                                                       ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                              144
                                                                                                                                                                                                                                                                                                  112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            composition comprising toxin e.g., ricin based antiviral compound 1 for treating viral infections such as human immunodeficiency
                                                                                                                                                                           25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303..565
/label= Ricin B chain
/note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                          Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                                                            97.9%; Score 951; DB 6; Length 565;
94.9%; Pred. No. 3.5e-93;
.ive 0; Mismatches 0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Linker peptide
/note= "Cleaved during activation of ricin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Castor bean preproricin protein (SEQ ID 1).
                                                                                                                                                2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..24
/label= Signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "N-glycosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25..290
/label= Ricin_A_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                             205 FOYIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                                                                                                                                                          FOYIEGEMRTRIRYNRRS 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302
                                                                                                              Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keener WK, Ward TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-581908/65.
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAI64137.
                                 565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG78300;
                                                                                                                                                                                                                                                                                                                                                                                              172
                                   Sequence
                                                                                                                                                                                                                                 52
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                                                                       Query Match
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                                                                                              Local
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The sequence relates to preproricin protein encoded by the DNA sequence given in AAA64137. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide nor-toxic to uninfected cells. The invention has anti-HIV and virucide ribosomes and enhancement of binding of the antiviral agent to galacrose residues on cell surfaces, and its cellular internalisation. The residues on cell surfaces, and its cellular internalisation. The and other viral infections, especially retroviral infections and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected antiviral agent is activated in viral particles or early-stage infected integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent enters all HIV susceptible cells, and one just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until degraded in it, unless the cell is infected with the virus, where the viral protease activates it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTOMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Proricin consists of the ricin A chain, a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide, and the ricin B chain. Proridin is proteclytically cleaved between the A chain and the linker to yield mature ricin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 IFPKQYPIINFTTAGALVQSYINFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency Virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 951; DB 22;
Pred. No. 3.5e-93;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chimeric - Ricinus communis
Chimeric - Human immunodeficiency virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292..303
/label= Linker_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Ricin A chain
/note= "N-glycosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG78304 standard; Protein; 565 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25..565
/label= Proricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 FQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205 FQYIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG78304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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296..297

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The sequence relates to the amino acid sequence of a modified preproricin protein encoded by AAI64145. The invention relates to a novel toxin protein encoded by AAI64145. The invention relates to a novel toxin coin calcin based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's mechanism of action is through inactivation of cellular ribosomes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITFLFTDVQNRYTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5. ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enhancement of binding of the antiviral agent to galactose residues on cell suxfaces, and its callular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-estage infected cells, Killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 84
                                                                                                                                                                                                                                                                                                                                                                                                                Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency
                   304..565
/label= Ricin B chain
/note= "GalacToSe/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.9%; Score 951; DB 22; Length 565; 94.9%; Pred. No. 3.5e-93; ive. 0; Mismatches 0; Indels 10
/label= HIV_protease_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 59-63; 66pp; English.
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                                                                                                                                                                                                                                                                      (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                                                                                     15-FEB-2001; 2001WO-US05282
                                                                                                                                                                                                                               16-FEB-2000; 2000US-0182759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                             Keener WK, Ward TE;
                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-581908/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          565 AA;
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAI64145
                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus infection.
                                                                                                      WO200160393-A1
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Matches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205
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AAP70326
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The full length sequences encoding ricin A (AAN70520), ricin D (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtained, using the messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70521, shows the nucleotide sequences of three plasmids containing cDNA inserts obtained by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA contagenesis may be used to place an ATG start codon and a Hindlif site at the beginning of the mature protein, (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors containing the PhoA promoter-operator and leader sequence (AAN70523) and suitable retroregulators.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 ELSNHABLSVTLALDVTNAYVVGYRAGNSAYFFHFDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 576;
                                                                                          Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                           Sequence of Ricinus communis (castor bean) Ricin toxin (RT or ricin) E precursor encoded by pRT38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.9%; Score 951; DB 8;
94.9%; Pred. No. 3.6e-93;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 14(1-2); 112pp; English.
                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                      /note= "A-chain"
315..576
/note= "B-chain"
                                                                                                                                                                                                        /note= "leader"
                                                                                                                                                                                                                                                                                                                                                                     86EP-0308877.
                                                                                                                                                                                                                                                                                                                                                                                                      86US-0837583.
(updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 188; Conservative
                                                                                                                                                                                                                          . 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1987-265177/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (CETU ) CETUS CORP. (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         576 AA;
                                                                                                                                           Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN70526
                                                                                                                                                                                                                                                                                                                                                                        13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-1986;
                                                                                                                                                                                                                                                                                                                                        23-SEP-1987.
 25-MAR-2003
                                                                                                               plant toxin
                  21-MAY-1991
                                                                                                                                                                                                                                                                                                        EP237676-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piatak M;
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                                                                                                                                                                                            Region
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AAP70326 standard; Protein; 576 AA.

AAP70326;

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156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This polypeptide comprises the castorbean cytotoxin, ricin.

DNA (see ALT91638) encoding the enzymatic A domain and a portion of the A-to-B linker peptide of ricin was used to construct a ricin-diphtheria toxin B' interleukin-2 gene that was expressed in E. coli. The hybrid protein can be isolated and used to treat conditions involving over-production of cells bearing IL2 receptors, such as certain T-cell lymphomas and organ transplant rejection crises. The hybrid inactivates ribosomes in cells bearing IL2 receptors, resulting in cessation of protein synthesis and death of target cells. Claimed hybrid proteins comprise a translocation of penalty and a cell binding domain from e.g. a hormone, growth factor or polypeptide toxin. The hybrid molecules can be used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New hybrid molecules for delivery of agents to cells - comprise binding domain of a cell binding ligand and a portion of a translocation domain of a protein
                                                                                                                                                                                                                                                    Ricin, cytotoxin, hybrid protein, cell delivery; cell binding ligand; translocation domain, diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Fig 11A-B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                        1..35
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                           AAW25787 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                 36..302
/label= A-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= B-domain
                          FOYIEGEMRTRIRYNRRS 189
                                               216 FQYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                              303..314
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0722484.
84US-0618199.
85US-0726808.
85US-0742554.
89US-0456095.
90US-0538276.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT91638.
                                                                                                                                                                                                                                                                                                              Ricinus communis.
                                                                                                                                                                                                                            Castorbean ricin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-TUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5668255-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1997
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                                                                                                                                                                                                27-MAR-1998
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                                                                                                                                                       AAW25787;
                            172
                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                 RESULT 14
                                                                                                                AAW25787
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111
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                                                                                                                                                                                                                                                                                                                                                                                                                      156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                               112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                                         36 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant, hybrid, binding domain, ligand, animal cell; diphtheria, translocation domain, botulinum, neurotoxin, ricin, cholera, tetanus; shiga-like toxin, pertussis, translocation, cytoplasmic membrane; HIV, cytosol, therapy; genetic deficiency disease; enzyme; co-factor; poison; adipocyte; cancer; virus; infection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant DNA molecule encoding a three part hybrid protein used in the treatment of Aids and genetic deficiency diseases -
                                                                                                                                                                                                                                                                                                                             52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                          -----VLPNRVGLPINORFILV
                                                                                                                                                                                                                          10; Gaps
delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition.
                                                                                                                                                                                     Query Match 97.9%; Score 951; DB 18; Length 576; Best Local Similarity 94.9%; Pred. No. 3.6e-93; Matches 188; Conservative 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                            2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY55892 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 FQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84US-0618199.
91US-0722484.
85US-0726808.
85US-0742554.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Castor bean ricin toxin.
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                                                                                                                                                        576 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY55892;
                                                                                                                                                          Seguence
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Example 4; Fig 11; 31pp; English.

therapy to affected cells, allowing them to function properly and alleviate or cure the disease. The hybrid is especially used in treating genetic deficiency diseases, by delivering to affected cells an enzyme supplying the missing function, to supplementing cellular levels of a particular enzyme or a scarce precursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as HIV, by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as detectable labels into cells. The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein toxin, an expected from diphtheria toxin, botulinum neurotoxin, ricin, cholera toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the castor bean ricin toxin sequence for use in generating the hybrid of the invention. The hybrid molecule enables the direction of appropriate

576 AA; Seguence

۲; 0; Indels 10; Gaps Query Match
97.9%; Score 951; DB 20; Length 576;
Best Local Similarity 94.9%; Pred. No. 3.6e-93;
Matches 188; Conservative 0; Mismatches 0; Indels 1

2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV

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96 ELSNHABELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155 52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95 d ò

156 GNYDRIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISBAAR 215 112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171 g

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Search completed: February 10, 2004, 16:22:27 Job time : 33.2239 secs

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Sequence 1, Appli
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Sequence 1, Appli
Sequence 27, Appli
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Sequence 74, Appl
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                                                                          (without alignments)
731.761 Million cell updates/sec
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                                                               February 10, 2004, 16:18:30; Search time 10.9281 Seconds
                                                                                                                       971
1 MIFPKQYPIINFTTAGATVQ......ARFQYIEGEMRTRIRYNRRS 189
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-485-286-27
5248666-4
US-08-318-303-16
US-09-338-793D-61
US-09-538-873-1
US-08-378-761A-77
US-08-485-286-77
US-08-488-113B-6
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US-07-901-707-1
US-07-988-430-1
US-08-425-336-1
US-08-488-1138-1
US-08-488-1138-1
US-08-488-1138-1
US-08-839-765-1
US-08-839-765-1
US-09-839-765-1
US-09-610-838-1
US-09-610-838-1
US-09-610-838-1
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US-09-610-838-6
US-08-378-761A-74
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                        328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                          OM protein - protein search, using sw model
                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                           US-10-083-336A-6
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Match Length DB
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Sequence 71,
Sequence 71,
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Huston, James S.
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
CORRESPONDENCE: 16
CORRESPONDENCE: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault STREET: Exchange Place, 53 State Street CITY: Boston STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.5%; Score 956; DB 2; Length 268; 95.0%; Pred. No. 7.1e-103; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/356,786

FILING DATE:

CLASSIFTCATION TATA:

PRIOR APPLICATION DATE:

APPLICATION NUMBER: 07/831,967

FILING DATE: 06-FEB-192

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 27,829

REPERENCE/DOCKET NUMBER: 27,829

REPERENCE/DOCKET NUMBER: 27,829

REPERENCE/DOCKET NUMBER: 27,829

REPERENCE/DOCKET NUMBER: 27,829

REPERENCE/DOCKET NUMBER: 27,829

REPERENCE/DOCKET NUMBER: 27,829

REPERENCE/DOCKET NUMBER: 28,93

TELEPHONE: (617) 248-7100

TELEPHONE: (617) 248-7100

INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                     US-08-184-237-4
US-08-482-920-4
US-08-484-341-4
US-08-483-502-4
US-09-726-651A-4
US-07-901-15
US-07-988-430-6
US-07-988-430-6
US-07-988-430-6
                                                                                                                                                                                            US-08-902-486-15
US-08-378-761A-71
                                                                                                                                         PCT-US92-09487-6
US-08-902-486-7
US-08-245-754A-2
                                                                                                                                                                                                                      US-08-485-286-71
                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1 n
                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08356786; Patent No. 5877305; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.0
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
             amino acid
TOPOLOGY:
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GGNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 170
                                                             63 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.9%; Score 951; DB 1; I 94.9%; Pred. No. 2.7e-102; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
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APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greta E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PATENTIN RELEGISE #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707 FILING DATE: 19920619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: No. 5376546and, Greta E. REGISTRATION NUMBER: 35,302
                                                                                                                                                                                                                                                             Sequence 1, Application US/07901707
Patent No. 5376546
                                                                                                                      171 RFQYIEGEMRTRIRYNRRS 189
                                                                                                                                                            183 RFOYIEGEMRIRIRYNRRS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (312) 346-5750
(312) 984-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (312) 984-575:
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 94.9
Matches 188; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                      VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 110
                                                                                                                                                                  111 GGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 170
                                                                                                                                                                                       61 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
                           ------VLPNRVGLPINQRFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosyputhetic Binding Protein for Cancer TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa Hurwitz, & Thibeault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
Exchange Place, 53 State Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
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          MIFPKOYPIINFTTAGATVOSYTNFIRAVRGRLT
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REGISTRATION NUMBER: 27,829
REGISTRAFOOCKET NUMBER: CRP-053
REBERONGUISTRATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08356786 Patent No. 5877305
                                                                                                                                                                                                                                                      171 RFQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                      181 RFQYIEGEMRTRIRYNRRS 199
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INFORMATION FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.0°
Matches 189; Conservative
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                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-356-786-10
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GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Unlie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 951; DB 1; I
Pred. No. 2.7e-102;
0; Mismatches 0;
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                      Sequence 1, Application US/08425336 Patent No. 5621083
                                                                                172 FOYIEGEMRTRIRYNRRS 189
                                                                                                                    181 FOYIEGEMRTRIRYNRRS 198
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TELEX: 25-3856
INCEMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ilarity 94.9%;
Conservative
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amino acid
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312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Thomas C. REGISTRATION NUMBER: P-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 188; Conserva
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COUNTRY: USA
ZIP: 60606-6402
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US-08-425-336-1
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                                                                                                                      APPLICANT: Better, Marc D.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Pin
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                     121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IFPROYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHBIPVLPNRVGLPINQRFILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION UMBER: US/07/988,430
FILING DATE: 19921209
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Pred. No. 2.7e-102;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRICE APPLICATION DATA:
APPLICATION UNBER: US 07/901,707
FILING DATE: 19-UTN-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: NO. 5416202and, Greta E. REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                    US-07-988-430-1
; Sequence 1, Application US/07988430
; Patent No. 5416202
; GENERAL INFORMATION:
                                                               172 FQYIEGEMRTRIRYNRRS 189
                                                                                                       181 FOYIEGEMRIRIRYNRRS 198
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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TELEX: 2
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Best Local
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61 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 267;
                                                                                                                                                                                                                                  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
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us-10-083-336a-6.rai

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Sequence 1, Application US/08477484B Patent No. 5756699
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TELEPHONE: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                       181 FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                          172 FOYIEGEMRIRIRYNRRS 189
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: USA
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121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 10; Gaps
                                                                                                                                                                                                                                                                        APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.9%; Score 951; DB 1; Length 267; 94.9%; Pred. No. 2.7e-102; Live 0; Mismatches 0; Indels
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FILING DATE: 19-UNN-1992
PRIOR APPLICATION DATA: US 07/787,567
APPLICATION DATA: US 07/787,567
FILING DAE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNI-Cholas, Janet M.
REGISTRATION NUMBER: 32,918
REPERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312,707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                E: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT--
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PELLING DATE: 07-JUN-1995
CLASSIPICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
APPLICATION DATA:
APPLICATION NUMBER: US 07/980,730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  Sequence 1, Application US/08488113B Patent No. 5744580 GENERAL INFORMATION:
                                                                                        181 FOYIEGEMRTRIRYNRRS 198
                                                 172 FOYIEGEMRTRIRYNRRS 189
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 188; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                    112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                    52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: El PO Compatible
COMPUTER: The PC compatible
COMPUTER: Patent PR PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 02-DEC-1992
FILING DATE: 09-DEC-1992
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500 West Madison Street, 34th floor
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UIN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
APPLICATION UNDHABE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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97.9%; Score 951; DB 1; Length 267;

Query Match

1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60

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REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 15-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 10-UNN-1992
ATTORNEY APPLICATION NUMBER: US 07/901,707
FILING DATE: 10-UNN-1992
ATTORNEY APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY APPLICATION NUMBER: US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 FOYIEGEMRIRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 FOYIEGEMRTRIRYNRRS 198
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                                                                                                                     97.98;
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                                                                                                                                                                      Matches 188; Conservative
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-646-360-1
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STREET: bou
CITY: Chicago
STATE: Illinois
                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                        52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                       112 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAAR 171
                                                                                                      1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRITTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                          -----VLPNRVGLPINQRFILV 51
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08646360

Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                              10;
  Pred. No. 2.7e-102;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                               2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT
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APPLICATION NUMBER: US/08/646,360
FILING DATE: 13 MAY-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/907,707
FILING DATE: UN 07/97,567
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                 181 FOYIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
     94.9%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 267 amino acids
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  Best Local Similarity 94.9
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STREET: 500
CITY: Chicago
STATE: Illinois
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US-08-646-360-1
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61 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDARAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                   112 GNYDRLEQIAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                 1 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILV
                                                         Indels 10; Gaps
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APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proceins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPAGEDOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
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Score 951; DB 2; I
Pred. No. 2.7e-102;
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500 West Madison Street, 34th floor
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENITON: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENITON: Proteins
NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                        Query Match
97.9%; Score 951; DB 3; Length 267;
Best Local Similarity 94.9%; Pred. No. 2.7e-102;
Matches 188; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                        2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----
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500 West Madison Street, 34th floor
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APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09136389
Patent No. 6146850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 FQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 FOYIEGEMRTRIRYNRRS 198
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Processins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDEWS Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%; Score 951; DB 3; Length 267; 94.9%; Pred. No. 2.7e-102; rative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-UUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAX-1996
APPLICATION NUMBER: PCT/US94/05348
                                                                          REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEPHONE: 312/707-9155
TELER: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
     US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 0 FILLING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.9%
Best Local Similarity 94.9%
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-09-136-389-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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97.9%; Score 951; DB 5; Length 267; 94.9%; Pred. No. 2.7e-102;
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                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                      CORRENT AFFILTANIAN PORTRER. PCT/US92/09487 ELING DATE: 19921104
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
                                                                          олькк: PCT/US92/09487
19921104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08378761A Patent No. 5635384 GENERAL INFORMATION;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WALSH, TERENCE A
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INA
TITLE OF INVENTION: PRECURSOR FO
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRESS:
ADDRESSEE: ANDRESS IN
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
STATE: IN
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION: TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 PQYIEGEMRTRIRYNRRS 189
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         IBM PC compatible
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I: 267 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US92-09487-1
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Best Local Similarity
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APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNKVGLPINQRFILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97.9%; Score 951; DB 4; Length 267; 94.9%; Pred. No. 2.7e-102; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGRWT INFORMATION:
NAME: MCNICALISM, US 07/87,567
FILING DATE: 312/707-9155
TELEFRONE: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9209487 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     172 FQYIEGEMRTRIRYNRRS 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TELER: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
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Best Local Similarity 94.99
Matches 188; Conservative
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-610-838-1
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RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
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                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                          2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 51
                                                                                                                             | IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
10; Gaps
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Search completed: February 10, 2004, 16:29:32
   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 290
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                       NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALICE E.R.
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TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                                                                                                                                                                                                                                                                                                                                                                        Length 290;
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPPLICATION NUMBER: US,08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDRER T
REGISTRATION NUMBER: 33651
                                                                                                                                                                                                                                                                                                                                                                                                            .
0
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Pred. No. 3e-102;
0; Mismatches 0
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; Patent No. 5646026
; Patent No. 5646026 5646119
                                                                                                                           REFERENCE/DOCKET NUMBER: 33651
REFERENCE/DOCKET NUMBER: 3827:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
                                                                                                                                                                                                                                                                                                                                                                          97.9%;
                                                                                                                                                                                                                                         LENGTH: 290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.9
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sn
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                                                                                                                                                                                                                                                                                                                                     US-08-378-761A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-485-286-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAAR 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97.9%; Score 951; DB 6; Length 290; 94.9%; Pred, No. 3e-102;
                                                                                                                                                                                                                                                                                                                                                   Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                Score 951; DB 1;
Pred. No. 3e-102;
0; Mismatches 0.
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0; Mismatches
          REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 290 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 49
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/535,636
FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 FQYIEGEMRTRIRYNRRS 189
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                                                                                                                                                                                                                                                                                                                                                   97.9%;
                                                                                                                                                                   : 290 amino acids
amino acid
BORUCKI, ANDREA T
                                                                                                                                                                                                                                                                                                                                                                                                      Matches 188; Conservative
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                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-485-286-27
                                                                                                                                                                                                                        STRANDEDNESS: single
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Job time : 10.9281 secs

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us-10-083-336a-6.rapb

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(without alignments)
1623.314 Million cell updates/sec
                                                                                                                                                                                                     February 10, 2004, 16:26:46; Search time 24.3781 Seconds
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_PUB_OPD:*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801455 segs, 209382283 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                          US-10-083-336A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                            Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 4, Appli Sequence 8, Appli Sequence 6, Appli Sequence 5, Al Sequence 10, Sequence 3, Al Sequence 1, Al Sequence 11, Sequence Sequence 3 Description Sequence US-10-083-336A-6 US-10-083-336A-1 US-10-083-336A-4 US-10-083-336A-8 US-10-083-336A-1 US-10-083-336A-1 US-10-083-336A-1 US-10-083-336A-1 US-10-083-336A-1 US-10-083-336A-1 US-10-083-336A-1 US-10-083-336A-1 US-10-083-336A-1 US-10-083-336A-1 US-10-083-336A-9 US-10-083-336A-9 US-10-083-336A-9 US-10-083-336A-9 US-10-083-336A-2 US-10-083-336A-2 US-10-083-336A-2 Query Match Length DB Score Result

Appli , Appl

Appli

Appli Appli Appli Appli Appli

Sequence 9, Appli Sequence 2, Appli Sequence 39, Appl

Seguence

									Sequence 5, Appli								Sequence 2	Seguence 9	Sequence 1 Seguence 1	Sequence 109,	5								
				12 US-10-375-209A-34		12 US-10-440-796-3		12 US-10-127-890-4	12 US-10-127-890-5	9 US-09-347-064-2	9 US-09-347-064-8	12 US-10-127-890-107	12 US-10-127-890-106	12 US-10-127-890-110	12 US-10-127-890-111	9 US-09-765-527-247	12 US-10-127-890-2	12 US-10-127-890-99	12 US-10-127-890-100	12 US-10-127-890-101	12 US-10-127-890-102	12 US-10-127-890-103	12 US-10-127-890-104	12 US-10-127-890-105	12 US-10-074-596-1	12 US-10-074-596-11	12 US-10-127-890-109	- 1	9 US-09-765-527-253
247	247	289	247	247	251	251	263	263	248	252	252	251	251	251	251	251	251	251	251	251	251	251	251	251	316	507	251	293	309
34.6	34.6	34.6	31.4	31.4	30.6	30.6	28.1	28.0	26.5	26.2	26.2	25.3	25.2	25.2	25.2	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.1	25.0	25.0	25.0
336	336	336	305	305	297.5	297.5	273	272	257.5	254	254	245.5	244.5	244.5	244.5	243.5	243.5	243.5	243.5	243.5	243.5	243.5	243.5	243.5	•	243.5			242.5
16	17	18	13	20	. 121	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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        Sequence 6, Application US/1008336A
Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAELS
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 971; DB 12; Length 189; Best Local Similarity 100.0%; Pred. No. 2.7e-103; Matches 189; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 TRIRYNRRS 189
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US-10-083-336A-6
US-10-083-336A-6
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1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAELSV 60
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                                                                                                                                                                                                                                                                                                                                                                    US-10-083-336A-8
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
                                                                                                          US-10-083-336A-11
Sequence 11, Application US/10083336A
Sequence 11, Application US/10083336A
Publication No. US2030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RILD 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
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100.0%; Pred. No. 2.7e-103;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 190
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    181 TRIRYNRRS 189
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Best Local Similarity
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Matches 189;
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64 ALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGN 123
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                                                                                                                                                                62 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                           122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
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Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPRENCE: P67452US(RIID) 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT APPLICATION OF 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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                                               61 TLALDVTNAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA
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98.5%; Score 956; DB 12; Length 18
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 186; Conservative 0; Mismatches 0; Indels
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APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods
FILE REFERENCE: F67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/10083336A
Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Richael P
TITLE OF INVENTION: Richael P
TITLE OF INVENTION: Richael P
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                              0; Indels 10; Gaps
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                                                                                 Length 199;
                                                                               Score 956; DB 12;
Pred. No. 1.5e-101;
                                                                                                                              0; Mismatches
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                                                                                     98.5%;
95.0%;
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TYPE: PRT ORGANISM: Ricinus communis
                                                                                                                              Matches 189; Conservative
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Best Local Similarity
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                             ; ORGANISM: R10
US-10-083-336A-5
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; Sequence 3, Application US/10083336A; Publication No. US20030181665A1; GENERAL INFORMATION:

US-10-083-336A-3

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61 BLSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Michael P
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
TILLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 198;
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COMPUTER: IBM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 37-Apt-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: McAndrews, Held & Malloy, Ltd. STREET: 500 West Madison Street, 34th floor CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 951; DB 12;
Pred. No. 5.7e-101;
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APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
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APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                      97.9%;
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COUNTRY: USA
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0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
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PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILLING DATE: 1999-03-30
UNDER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
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                                                                                                                                         172 PQYIEGEMRTRIRYNRRS 189
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNOEDAEAITHLFTDVONRYTFAFG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
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APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452080 (RIID 01-58)
CURRENT APPLICATION NUMBER: USINJ0/083,336A
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --VLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 10; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.9%; Score 951; DB 12; Length 267; Best Local Similarity 94.9%; Pred. No. 8.7e-101; Matches 188; Conservative 0; Mismatches 0; Indels 10
                    FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MONICHOLAS, Janet
REGISTATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-9155
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/10083336A; Publication No. US20030181665A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           LENGTH: 267 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 FQYIEGEMRTRIRYNRRS 189
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.1
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ORGANISM: Ricinus communis
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APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANG
TITLE OF INVENTION: COMPANS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 113
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                                                                                                                            156 GNYDRLEQLAGNIRRINIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                  112 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
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APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPERBNCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
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Pred. No. 8e-100;
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Sequence 2, Application US/10083336A; Publication No. US20030181665A1; GENERAL INFORMATION:
                                                                                                                                                                               ; Sequence 9, Application US/10083336A; Publication No. US20030181665A1
                                        174 YIEGEMRTRIRYNRRS 189
                                                                               183 YIEGEMRIRIRYNRRS 198
                                                                                                                                                                                            FULLICATION NO. US20030181665A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Ricinus communis
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                                                                                                                                                                                                                                             APPLICANT: Olson, Mark A
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                                                                                                                                           RESULT 13
US-10-083-336A-9
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APPLICANT: VITETA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROME (VLS)
TITLE OF INVENTION: SYNDROME (VLS)
CURRENT APPLICATION NUMBER: US/10/440,796
CURRENT PELING DATE: 2003-05-19
PRIOR FILING DATE: 2000-03-30
PRIOR PILING DATE: 1999-03-30
NUMBER: 60/126,826
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 113
                                                                                                                                                                                                                                                                                                                                                                                         SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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                                                                                                                                                                                                                                                                   4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-------ULPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                               3 PKQYPIINFTTAGATVQSYINFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                          Gaps
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                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                            10;
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                                                                                                                                                                                 96.9%; Score 941; DB 12; Length 267; 94.9%; Pred. No. 1.2e-99;
                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 941; DB 12;
Pred. No. 1.2e-99;
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                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 YIEGEMRTRIRYNRRS 189
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94.9%;
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SEQ ID NO 1
LENGTH: 267
TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 186; Conservative
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                                                                                                                                                                                                       Best Local Similarity 94.9
Matches 186; Conservative
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Best Local Similarity
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                                                                                                                                                                                    Query Match
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58 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 117
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123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Nobert W
APPLICANT: Wannemacher, Nobert W
ATTILE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Milard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemcher, Robert W
AITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEO ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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96.8%; Score 939.5; DB 12; Length 185;
Best Local Similarity 98.4%; Pred. No. 1.1e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.9%; Score 679; DB 12; Length 179; 93.1%; Pred. No. 9e-70; ive 0; Mismatches 0; Indels 10
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RESULT 15
US-09-792-793A-39
Sequence 39, Application US/09792793A
Sequence 30, Application US/09792793A
Sequence No. US20020168370A1
SEQUENCE NO. US20020168370A1
SERVERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 118
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                                                                                                     52 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
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                             36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-------VLPNRVGLPINQRFILV 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.6%; Score 336; DB 10; Length 247;
Best Local Similarity 38.9%; Pred. No. 3.7e-30;
Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 10, 2004, 16:53:53 Job time: 25.3781 secs
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                                                                                                                                                                                                      112 GNYDRLEQLAGNLRENIELGNGPL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 39
LENGTH: 247
TYPR: PRT
CRGANISM: Trichosanthews kirilowii
US-09-792-793A-39
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171 IGKRV 175
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 10, 2004, 16:17:35; Search time 10.2276 Seconds (without alignments) 1777.145 Million cell updates/sec

US-10-083-336A-6

Title: Perfect score:

971 1 MIFPKQYPIINFTTAGATVQ.....ARFQYIEGEMRTRIRYNRRS 189 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	ricin D precursor	i,		abrin-d precursor	abrin-c precursor		karasurin-B - Tric	karasurin C - Tric	abrin-b precursor	abrin (clone 7.2)	abrin-a precursor	beta-luffin - smoo	lúffin-b - smooth	rRNA N-glycosidase	rRNA N-glycosidase	agglutinin I precu	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	mistletoe lectin I		rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	antiviral protein	rRNA N-glycosidase		rRNA N-glycosidase	rRNA N-glycosidase
SUMMARIES	ΩI	RLCSD	RLCSAG	RLTZT	532431	S16022	JU0393	JC5032	JC5606	S32430	C39761	TZLSA	823519	JN0108	S22494	RLPUGG	S62627	S25560	JC4840	JC4235	PD0018	JT0753	S28421	A39817	S17757	JE0401	T12573	JC4811	2	S28539
	DB	1	Н	Н	7	7	7	C4	7	7	7	Н	7	7	7	Н	7	7	7	71	7	7	7	7	α	7	7	۲3	7	7
	Length	576	564	289	528	562	247	247	289	527	251	528	278	250	277	286	570	286	245	286	254	316	294	278	313	261	289	272	253	253
d	Query Match	97.9	88.7		'n	w.	33.6	Ψ,	~	33.3	ςi.	_;	ς:	ď	28.3	m	œ.	28.0	7.	۲.	27.2	'n.	19.2	17.9	7.	17.4	15.3	14.2	13.5	13.1
	Score	951	861.5	336	327.5	327.5	326	326	326	323	310.5	303.5	300.5	293.5	274.5	273	273	272	270	265	264	243.5		174		168.5	48.	138	131	127
	Result No.		2	ጠ	4	Ŋ	9	7	80	б	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27		29

rRNA N-glycosidase	ribosome-inactivat	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	tritin - wheat	rRNA N-glycosidase	rRNA N-glycosidase	protein synthesis	rRNA N-glycosidase	hypothetical prote	shiga-like toxin I	Shiga toxin 2 subu	Shiga toxin 2 subu	Shiga-like toxin I
\$29931	S46239	805205	S28541	RLQHG2	S17519	S33631	A58923	RLBH	JC5848	S17932	S21940	I54695	E90779	G85640	801032
7	C)	7	7	Н	~	N	N	۲	7	7	7	~	7	~	7
253	310	283	253	292	293	275	253	280	280	236	319	319	319	319	318
13.1	12.9	12.8	12.7	12.5	12.0	11.9	11.8	11.7	11.5	11.3	11.2	11.1	11.1	11.1	11.1
127	125	124	123	121	116.5	116	115	114	112	110	109	108	108	108	107.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 RICSD	
ricin D precursor - castor bean N;Contains: rRNA N-qlycosidase (EC 3.2.2.22)	
C;Species: Ricinus communis (castor bean)	
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999	
C; Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903	
R; Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.	aver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985	
A, Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.	ommunis.
A; Reference number: A24041; MUID:86067214; PMID:2999712	-
A;Accession: A24041	-
A; Molecule type: DNA	
A;Residues: 1-576 <hal></hal>	
A; Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083	
R;Tregear, J.W.; Roberts, L.M.	
Plant Mol. Biol. 18, 515-525, 1992	
A,Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene a	ricin gene ¿
A;Reference number: S20513; MUID:92163016; PMID:1371405	

A; Accession: S20513

A; Molecule type: DNA A; Residues: 1-576 <TRE>, A; Cross-treences: 1-576 <TRE. A; Cross-treences: Experts, L.M.; Lord, J.M. R; Lamb, F.I.; Roberts, L.M.; Lord, J.M. Bur. J. Biochem. 148, 265-270, 1985 A; Title: Nucleotide sequence of cloned cDNA coding for preproricin. A; Reference number: A24614; MUID: 85179479; PMID: 3838723

A;Molecule type: mRNA A;Residues: 12-75, 10', 77-550, 18', 552-576 <LAM> A;Residues: 12-75, 10', 77-550, 18', 10'; 21007; PIDN:CAA26230.1; PID:g21078 A;Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078 R;Yoshitake, S.; Funatsu, G.; Punatsu, M. R;Yoshitake, S.; Funatsu, G.; Punatsu, M. A;Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile challence number: A03372

A; Accession: A03372

A,Molecule type: protein
A;Residues: 36-97, °0', 99-109, °S',111-269, °D',272-283, °L',285-288,290-302 <YOS>
A;Residues: 16-97, °0', 99-109, °S',111-269, °D',272-283, °C',285-288,290-302 <YOS>
A;Note: this paper cites the others in the series providing experimental details for the R;Araki, °C', Punatsu, G.
FEBS Lett. 191, 121-124, 1985
A;Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan

A;Reference number: A24010 A;Accession: A24010

A,Molecule type: protein A,Residues: 315-383, Ps', 386-576 <ARA> A;Punatsu, G.; Kimura, M.; Funatsu, M. Agric. Biol. (hem. 43, 2221-2224, 1979 A,Title: Primary structure of Ala chain of ricin D.

A; Reference number: A03374

A;Accession: A03374 A;Molecule type: protein

R;Araki,

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A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',4d527,'E',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>A;Note: this paper, one of a series, summarizes the experimental details for the determi R;Ready, M.P.; Kim, Y.; Robertus, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;215/Active site: Arg #status predicted
F;294-318,334-233,377-394,465-418,504-521/Disulfide bonds: #status experimental
F;236,349,360/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status experimental
F;548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental
                                                                                                        Proteins 10, 270-278, 1991
A,Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism A,Reference number: A48237; MUID:91352006; PMID:1881883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Ricinus communis (castor bean)
C;Decies: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A24261; A24210
R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J. Biol. Chem. 260, 15682-15686, 1985
A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin. A;Reference number: A24261; MUID:86059449; PMID:2999130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-564 <ROB>
A;Cross-references: GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
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                                                                                                                                                                                                                                                  Proteins 10, 260-269, 1991
A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.9%; Score 951; DB 1; Le
94.9%; Pred. No. 2.7e-79;
Niematrohes 0;
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                                                                                                                                                                                             A, Contents: annotation; active site R; Rutenber, E.; Robertus, J.D.
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Matches 188; Conserv
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A.Cross-references: GB:M34858; NID:g170536; PIDN:AAA34207.1; PID:g170537
A.Experimental source: tuber
R.Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A.Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rib
A.Reference number: A36274; MUID:90256790; PMID:2341400
T.; Yoshioka, Y.; Funatsu, G.
Biophys. Acta 872, 277-285, 1986
The complete amino acid sequence of the B-chain of the Ricinus communis aggluti:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolian s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: alpha-TCS; type I ribosome-inactivating protein
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1988 #sequence revision 26-Jan-1996 #text_change 23-Mar-2001
C;Accession: JUD566; 336274; JC1093; A36273; JT0003
R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.
Gene 97, 267-272, 1991
A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 ELSNHAELSVILALDVINAYVVGCRAGNSAYFFHPDNOEDAEAITHLFTDVQNSFTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 IPPKQYPIINFTTADATVESYTNFIRAVRSHLTTGADVRHEIPVLPNRVGLPISQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDABALTHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;536,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A'Residues: 1-233,'T',235-246,'M',248-289 <CHO>
A'Cross-references: GB-10544; NID:9170534; PIDN:AAA34206.1; PID:9170535
R;Zheng, H.G.; Mang, B.; Shao, P.Z.; Yang, X.R.
Acta Genet. Sin. 21, 42-51, 1994
A;Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A;Reference number: JC1093; MUID:94271613; PMID:8003348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.7%; Score 861.5; DB 1; Length 564; 86.9%; Pred. No. 4.2e-71; ive 7; Mismatches 8; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: JT0566; MUID: 91153657; PMID: 1999291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 FOYIEGEMRTRIRYNRRS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 172; Conservative
                                                                           A;Reference number: A24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-289 <SHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JT0566
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                                                                                                             A;Accession: A24210
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A; Accession: JT0003

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Cydres 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
Cydcession: S32431; S34408
Cydcession: S32431; S34408
RyHung, C.H.; Lee, H.C.; Lin, J.Y.
RyHung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
Ayreference number: S32429; MUID:93132798; PMID:8421313
Ayreference number: S32429; MUID:93132798; PMID:8421313
Ayreference number: S32431
Ayreference number: S32431
Ayreferences: GB:M98346
Ayreferences: GB:M98346
Ayreferences: GB:M98346
Ayreferences: GB:M98346
Sylvang, C.; Lee, M.; Lee, T.; Lin, J.
Submitted to the BMBL Data Library, March 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating. The A and B chains are linked by a single disulfide bond, which is essential for toxicit C;Superfamily: rich; rRNA N-glycosidase homology C;Reywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p) F;1-251/Product: abrin-d chain A #status predicted ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chair A;Reference number: $16022; MUID:91266957; PMID:2050149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating The A and B chains are linked by a single disulfide bond, which is essential for toxicit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F)7-246/Domain: FRNA N-glycosides homology cRNG>
F)7-246/Domain: FRNA N-glycosides homology cRNG>
F)261-528/Product: abrin-d chain B #status predicted <BGH>
F)283-325,326-336,369-407,414-449,453-492,495-528/Region: 40-residue repeats
F)1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F)1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F)74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F)200,253,381,401,442/Binding site: carbohydrate (Asn) (covalent) #status predicted
F)247-269,286-305,329-344,17-330,456-473/Disulfide bonds: #status predicted
F)288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F)500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QDQVIKFTTEGATSQSYKQFIBALRQRLTGGLIHDIPVLPDPTTVEERNRYITVELSNSE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1562 <WOO>
A;Cross-references: EMBL:X55667; NID:g16084; PIDN:CAA39202.1; PID:g16085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 528;
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43.9%; Pred. No. 3.6e-22;
tive 22; Mismatches 68; Indels
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Eur. J. Biochem. 198, 723-732, 1991
A;Title: Preproabrin: genomic cloning, characterisati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-169,'C',171-320,'L',322-528 <HU2>
A;Cross-references: GB:M98346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
Species: Abrus precatorius (Indian licorice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 QYPIINFTTAGATVQSYTNFIRAVRGRLT-
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nes 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S34408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 EMRTRIR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Status: preliminary
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F.24-270/Product: trichosanthin alpha #status experimental <MAT>
F.27-266/Domain: rRNA N-glycosidase homology <RNG>
F.271-286/Domain: rRNA N-glycosidase homology <RNG>
F.371-286/Domain: rRNA N-glycosidase homology <RNG>
F.371-286/Active site: Tyr, Glu, Arg #status predicted
                                                                                                                                                                                                                                                                   A;Accession: A3621.
A;Molecule type: protein
A;Residues: 24-270 cCOL>
B;Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pure Appl. Chem. 58, 789-798, 1986
A;Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
A;Reference number: JT0003
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                           A; Residues: 1-72, 'V', 74-90,'S', 92-233,'T', 235-267,'D', 269-289 <ZHB>
A; Cross-references: GB:S70176; NID:9547148; PIDN:AAB31048.1; PID:9547149
R; Collins, B.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan J. Biol. Chem. 265, 8665-8669, 1990
A; Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abr A; Reference number: A36273; MUID:90256789; PMID:2341399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 24-56,'L',58-59,'I',61-71,'I',73-81,85-86,'L',88-92,'DAGLPRNAVL',93-142,'GL'
A;Experimental source: tuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-8;Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y. submitted to the Brookhaven Protein Data Bank, July 1994
A;Reference number: A67092; PDB:1MRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Xiong, J.P.; Xia, Z.X.; Wang, Y.
submitted to the Brookhiaven Protein Data Bank, December 1994
A;Reference number: A66711; PDB-1TCS
A;Concents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rixiong, J.P.; Xia, Z.X.; Wang, Y. Nat. Struct. Biol. 1, 695-700, 1994 A; Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution A; Reference number: A58622; MJID:95360714; PMID:7634073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with formycin, residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNKYTFAFGGNYDRLE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --RVGLPINQRFILVELSNHAEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation; X-ray crystallography, 1.6 angstroms,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y. submitted to the Brookhaven Protein Data Bank, July 1994 A;Reference number: A67091; PDB:1MRJ
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42; Mismatches

72; Conservative

Matches

Query Match Best Local Similarity

A; Gene: tcs C; Genetics: C; Function: 10 INFTTAGATVQSYTNFIRAVRGRLTVLPN----

abrin-d precursor - Indian licorice (fragment) N; Contains: rRNA N-glycosidase (EC 3.2.2.22)

179 MRTRI 183

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72; Conservative
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C; Superfamily: ricin; rRNA N-glycosidase homology
C; Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
F;35-286/Product: abrin-c chain A #status predicted <ACH>
F;41-280/Domain: rRNA N-glycosidase homology <RNG>
F;295-562/Product: abrin-c chain B #status predicted <BCH>
F;295-562/Product: abrin-c chain B #status predicted <BCH>
F;397-359,360-400,403-441,448-483,487-526,529-562/Region: 40-residue repeats
F;367-400,403-441,448-483,485-756,529-562/Region: 40-residue repeats
F;317-359,330/Bainding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;108,201/Active site: Glu, Arg #status predicted
F;108,201/Active site: Glu, Arg #status predicted
F;281-303,320-339,363-380,451-464,490-507/Disulfide bonds: #status predicted
F;321,387,436,485-481-484,490-507/Disulfide bonds: #status predicted
F;332,346/Bainding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               karasurin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 ERWAHQTREEISLGLQALTHAIS---FIRSGASNDEEKARTLIVIIQMASEAARYRYISN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
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Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
Cipate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.7%; Score 327.5; DB 2; Length 5 43.9%; Pred. No. 3.9e-22; Live 22; Mismatches 68; Indels
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82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 EMRTRIR 184
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C;Accession: JC5032
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Rikondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Rilol. Pharm. Bull. 19, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka.
A;Reference number: JC5032; MUID:97108848; PMID:8951169
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A;Residues: 22-270 <KON>
C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
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Blol. Pharm. Bull. 19, 1465-1499, 1996
A.fitle: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka A.Reference number: JCS032; MUID:97108848; PMID:8951169
                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-247_kKON>

C;Coment: This protein belongs to type I ribosomal-inactivating proteins which catalyti:
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: DDBJ:AB000666; NID:g2329830; PIDN:BAA21786.1; PID:g2329831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Contains: karasurin A
C;Species: Trichosanthes kirilowii var. japonica
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 19-Jul-2002
                             C;Species: Trichosanthes kirilowii var. japonica
C;Date: 27-Feb_1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Mismatches 50; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 289;
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39.6%; Pred. No. 2.3e-22;
Live 44; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rimizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
A;Title: Cloning and bacterial expression of a gene enco
A;Reference number: JC5606; MUID:97356562; PMID:9212998
A;Accession: JC5606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 326; DB 2;
Pred. No. 1.9e-22;
karasurin-B - Trichosanthes kirilowii var. japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               karasurin C - Trichosanthes kirilowii var. japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.6%;
39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.6%
Best Local Similarity 39.6%
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: JC5606; JC5033
                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-247 <KON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-289 <MIZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 RV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 RI 183
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Gaps

16;

173 RVGVSIRTN 181

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A,Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Cor A,Reference number: S32429; MUID:93132798; PMID:8421313
                                                                                                                                                                                                                                                                                                                                                                     R;Evensen, G.; Mathiesen, A.; Sundan, A.
Dalol. Chem. 266, 8848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A;Reference number: A39761; MUID:91201329; PMID:2016300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 'M', 1-251 < EV2>
A; Residues: 'M', 1-251 < EV2>
A; Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C; Superfamily: ricin; rRNA N-glycosidase homology
C; Reywords: duplication; glycosidase; hydrolase; lectin; toxin
F; 7-225, Product: abrin (clone 7.2) chain A #status predicted <ACH>
F; 7-246/Domain: rRNA N-glycosidase homology <RNS
F; 7-246/Domain: rRNA N-glycosidase homology <RNS
F; 7-4,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F; 164,167/Active site: Glu, Arg #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 INFTTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Cross-references: GB:M98344; NID:gl66294; PIDN:AAA32624.1; PID:gl66295
A;Note: the coding region for the sequence shown is preceded by an ATG codon
A;Note: residues 1-8 were derived from the synthesized primer
A;Note: residues 1-8 were derived from the synthesized primer
A;Frunatsu, G:, Taguchi, Y:, Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abrin-a precursor - Indian licorice (fragment)
N;Contains: RRNA N-Gylvosidase (EC 3.2.2.2)
C;Specias: Abrus precatorius (Indian licorice)
C;Specias: 31-Dec-1993 #sequence revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: S32429; JUC022, Ä39761; JC1398; S14472; S24133; S74110; S74111
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
                                                                                                                                                                                                                                                                        C,Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999 C;Accession: C39761; S14471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 İKFSTEGATSQSYKQFIEALRERLRGGLIHDIPVLRDPTTVEERNRYİTVELSNSERESI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-251 <EVE>
R;Rvensen, G; Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32.0%; Score 310.5; DB 2; Length 251; 43.2%; Pred. No. 5e-21;
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    Indian licorice (fragment)

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                                                                                                                                                                                             N.Contains: rRNA N-glycosidase (EC 3.2.2.22)
C,Species: Abrus precatorius (Indian licorice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown
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Best Local Similarity 43.2<sup>1</sup>
Matches 79; Conservative
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A; Residues: 'E', 2-528 <HUN>
                                                                                                                                                     abrin (clone 7.2) precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S14471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 SIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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                                                                          RESULT 10
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(Species: Abrus precatorius (Indian licorice)
(Species: Abrus precatorius (Indian licorice)
(Species: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
(Spacession: 832430; UC1399)
(R; Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
(Mol. Biol. 229; 263-257; 1993)
(A; Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. CC
A; Reference number: 832429; MUID:93132798; PMID:8421313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxid
A;Reference number: JC1398; MUID:93169023; PMID:7763422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Molecule type: protein
A; Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430
A; Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430
A; Experimental source: seed
C; Superfamily: ricin; rRNA N-glycosidase homology
C; Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F; F1-250/Product: abrin-b chain A #status predicted <ACH>
F; 7-245/Domain: rRNA N-glycosidase homology <ARNG>
F; 260-527/Product: abrin-b chain B #status experimental <BCH>
F; 282-3245, 325-365, 368-4448, 452-491, 494-527/Region: 40-residue repeats
F; 1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F; 74, 113, 194, 195/Binding site: substrate (Ann) (covalent) #status predicted
F; 163, 166, 440/Binding site: substrate (Ann) (covalent) #status predicted
F; 163, 166, 440/Binding site: substrate (Ann) (covalent) #status predicted
F; 163, 166, 440, 161-340, 441, 452, 452, 472/Pisulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 ELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYIDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 EQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 ERLARQTRQQIPLGLQALRHALSFL----QSGTDDQELARTLIVIIQMASBAARYRFISY 172
                                                                                                                                                                                                                                                                                                                                                                                  142 GKIRENIPLGLPALDSAITTLFYYNAN----SAASALMVLIOSTSEAARYKFIEOOIGK 196
                                                                                                                                                              63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                              85 VAIDVTNVYVMGYRAGDISYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQIAA 141
                                                                                                                                                                                                                                                                                                                             GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
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                                                ---GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted F;499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%; Score 323; DB 2; Length 527; 43.9%; Pred. No. 9.2e-22; Live 21; Mismatches 69; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abrin-b precursor - Indian licorice (fragment)
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    10 INFTTAGATVQSYTNFIRAVR--
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Best Local Similarity
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A; Residues: 1-527 <HUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 RI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 kV 198
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30.2%; Score 293.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 RTRIRYN 186
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A;Molecule type: protein
A;Residues: 1-250 <1SL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     luffin-b - smooth loofah
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Best Local Similarity
Matches 66; Conserv
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A; Residues: 1-278 < KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 RTRIR 184
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A, Accession: S74110; MUD19700945; FMID18950059
A; Rocession: S74111
A; Rocession: S74111
A; Rocession: S74111
A; Molecule type: protein
A; Residues: 262-106;154-172
A; Experimental source: seed
A; Accession: S7411
A; Molecule type: protein
A; Residues: 262-276; X'.278-280;329-348;369-388;399-418 < LIW>
A; Experimental source: seed
A; Accession: S7411
A; Molecule type: protein
A; Residues: 262-276; X'.278-280;329-348;369-388;399-418 < LIW>
A; Experimental source: seed
C; Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inh taining receptors on the cell surface. The A and B chains are linked by a single disulfice; Superfamily: ricin; rRNA N-glycosidase homology
C; Reywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid; F; 1-251, Product: abrin-a chain A #status experimental ACH>
F; 246, Domain: rRNA N-glycosidase homology < RNG>
F; 261-528/Product: abrin-a chain B #status experimental ACH>
F; 283-325, 236-366, 369-407, 414-449, 453-492, 495-528/Region: 40-residue repeats
F; 11, Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F; 14, 167/Active site: Glu, Arg #status predicted
F; 14, 167/Active site: Glu, Arg #status predicted
F; 281, 226, 286-305, 329-346, 417-430, 456-473/Disulfide bonds: #status predicted
F; 281, 212/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F; 500, 521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:X54872
A;Note: residues 1-8 were derived from the synthesized primer
A;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biotechnol. Biotchem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxio
A;Reference number: JC1398; MUID:93169023; PMID:7763422
                                                                                                                                          A; Molecule type: protein
A; Residues: 1-201,203-251 <FUN>
A; Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
R; Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A; Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A; Reference number: A39761; MUID:91201329; PMID:2016300
A,Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein frd
A,Reference number: JT0202
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A)Accession: JC1398
A)Accession: JC1398
A)Accession: JC1398
A)Residues: 261-347, T',349-351,'A',353-357,'L',359-528 «KIM»
A)Experimental source: seed
A)Experimental source: seed
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B)Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
B)Choly M, LD: Truggita, A.; Lin, J.Y.
FEBS Lett. 309, 115-118, 1992
B)Experimental source: S14471
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Best Local Similarity 41.1%; Pred. No. 5.7e-20;
Matches 76; Conservative 26; Mismatches 64; Indels 19; Gaps
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A; Molecule type: protein
A; Residues: 262-297, Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 < CHE>
R; Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Bur. J. Biochem. 240, 564-569, 1996
A; Title: Probing the domain structure of abrin-a by tryptic digestion.
A; Reference number: 874110; MUID: 97008945; PMID: 8856055
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A,Reference number: S24133; MUID:92371656; PMID:1505674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 'E',2-251 <EVE>
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                                                                                                                A; Accession: JT0202
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C;Species: Inffa cylindrica (smooth loofah)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
R;Acceoka, 0:; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
Plant Mol. Biol 19, 887-889, 1992
Plant Mol. Biol 19, 887-889, 1992
A;Titles Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating A;Reference number: S23519; MUID:92353400; PMID:1643290
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Agric. Biol. Chem. 55, 229-238, 1991
Agric. Biol. Chem. 55, 229-238, 1991
Afritle: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from A;Reference number: JN0108; MUID:91248488; PMID:1368666
A;Accession: JN0108
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                                                                                                                                                                        62 TLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 119
                                                                                                                                                                                                                                                            65 EVGIDVĪNAYVVAYRĀGTQSYFLRDAPSSASD----YLFTGT-DQHSLPFYGTYGDLER 118
                                                                                                                                                                                                                                                                                                                                                     120 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 179
                                                                                                                                                                                                                                                                                                                                                                                                        119 WAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S1 AITWAIDVINVYIMGYLVNSTSYFF---NESDAKLASQYVFKGSTIVTLPYSGNYERLQN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       || :|| || || :||:||:||:|::|
138 AAGKVREKIPLGFRAFDSAITSLFHYDS----TAAAGAFLVIIQTTAEASRFKYIEGQI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
                                                        C;Species: Luffa cylindrica (smooth loofah)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
C;Accession: JN0108
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10 INFTTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV
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C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;26-264/Domain: rRNA N-glycosidase homology <RNG>
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F;5-246/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.9%; Score 300.5; DB 2;
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DB 2; Length 250;

Query Match

us-10-083-336a-6.rpr

Page 7

Peet Local Similarity 33.7%, Pred, No. 1.66-19, Matches 51, Conservative 46; Manaaches 57; Indess 21, daps 4, Matches 51, Conservative 46; Manaaches 57; Indess 21, daps 4, DD NTTHACATORYMERIANDROM	10 INFTINGATIVOSTINGITANEGRITYLERNUGENINORFILITEIGNING 77 2 VARSESSENINGSTREELEN
F;48,53,97,104,225,246/Binding site: carbohydrate (Asn) (covalent) #status experimental F;90,179,182/Active site: Tyr, Glu, Arg #status predicted Query Match 277;	A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 24-77, "R',79-132," C;Punction: Annotion: A,Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA there C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
Similarity 33.3%; Pred. No. 1.1e-17; 3; Conservative 42; Mismatches 61;	<pre>C;Keywords: glycoprotein; glycosidase; hydrolase; lectin; seed; toxin F;1-18/Domain: signal sequence #starus predicted <sig> F;19-23/Domain: amino-terminal propeptide #status predicted <pro></pro></sig></pre>

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F;24-269/Product: rRNA N-glycosidase alpha-momorcharin #status experimental <MAT>F;27-266/Domain: rRNA N-glycosidase homology <RNG>F;270-286/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;370-286/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;33,183,186/Active site: Tyr, Glu, Arg #status predicted F;250/Binding site: carbohydrate (Asn) (covalent) #status experimental
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Query Match	Query Match	28.1%; Score 273; DB 1;	Score	273; Di	3 1; L	28.1%; Score 273; DB 1; Length 286;				
Matches	Describoral Similarity 31.0%; Figu. NO. 1.0651/; Matches 63; Conservative 40; Mismatches 62; Indels 16; Gaps	ative 4	o, Mis	matches	62;	Indels	16;	Gaps	4;	
δy	10 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAELSVT 62	SYTNFIRA	VRGRLTV	LPNRVGL	I	NORFILV	ELSNH	AELSVT	62	
, qa	25 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 84	RSYGMFIKD	: LRNALPF	: REKVYNI!	: 	SGAGRYLLM	:: : : YLLMHLFNYI	GKTIT	84	

197 R 197

ð g Search completed: February 10, 2004, 16:28:01 Job time : 10.2276 secs

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¹⁸² R 182

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Pebruary 10, 2004, 16:13:55 ; Search time 6.30467 Seconds
 (without alignments)
 1409.756 Million cell updates/sec Run on:

US-10-083-336A-6 971 1 MIFPKQYPIINFTTAGATVQ......ARFQYIEGEMRTRIRYNRRS 189 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ption	PO2879 ricinus com PO6750 ricinus com PO6750 abrus preca P28590 abrus preca P28590 abrus preca P28590 abrus preca P28590 abrus preca P28591 bryonia dio P33185 bryonia dio P31183 sambucus ni P31184 bryonia dio P11140 abrus preca P22851 luffa cylin Q9ffx4 cucumis fig Q00465 luffa cylin P16094 momordica c P29339 momordica b P13186 gelonium mu Q03465 phytolacca P21326 mirabilis J P1227 phytolacca P21326 mirabilis J P21326 mirabilis G41391 saponaria o Q41391 saponaria o Q40772 phytolacca P2136 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o P27560 saponaria o
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* Query Match Length	250 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
% Query Match	888.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0
Score	951 961.5 32.736 32.736 32.736 32.736 32.736 30.7.55 30.7.55 30.7.56 30.7.
Result No.	11111111111111111111111111111111111111

P28522 zea mays (m P25892 zea mays (m P08092 bacteriopha P10149 bacteriopha 067411 aquifex aeo Q00531 hordeum vul P7525 mycoplasma Q9bxb4 homo sapien P24153 vibrio chol P27561 saponaria o Q00971 vibrio prot P44755 haemophilus
RIPX MAIZE RIP9 MAIZE RIP9 MAIZE SITA BPH19 SITA BPH10 SYV ĀQUAE Y16 HORVU Y348 MYCPN ORPH HUMAN RIP4 VIBCH RIP4 SADOF NPRV VIBCH RIP4 SADOF
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ALIGNMENTS

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Toxicon 39:1723-1728(2001).
                    Proteins 10:251-259(1991)
                                       "X-ray structure of
                                                            Robertus J.D.
                                                                  MUTAGENESIS
"Ricin."
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14-JAN-98.
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1APG; 31-JAN-94.
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**Analysis of several key active site residues of ricin A chain by

**Analysis of several key active site residues of ricin A chain by

**Analysis of several key active site residues of ricin A chain by

**Tay Crystallography.";

**Protein Eng. 5:775-779(1992).

**C. !- FUNCTION: Ricin is higly toxic to animal cells and to a less

**Extent to plant cells. The A chain is responsible for inhibiting

protein synthesis through the catalytic inactivation of 608

**Tibosomal subunits. It acts as a glycosidase that removes a

specific adenine residue from an exposed loop of 288 ribosomal

RNA. As this loop is involved in the binding of elongation

factors, the modified ribosomes are unable to support protein

synthesis. The A chain can inactivate a few thousand ribosomes

per minute, thus inactivating them faster than the cell can make

new ones. A single A-chain molecule can therefore kill an animal

cell. The B chain binds to cell receptors and facilitates the

cell. The cell of the A chain; B chains are also responsible

for cell agglutination (lectin activity). It binds to beta-D-

galactopyranoside moieties.

C. -- GATALYTITY. ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
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SUBUNIT: Disulfide-linked dimer of A and B chains.
DOMAIN: THE B chain is composed of two domains, each domain consists of 3 homologue subdomains (alpha, beta, gamma).
PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN PAMILY: TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -ray structure of recombinant ricin A-chain at 1.8-A resolution."; Mol. Biol. 244:410-422(1994).
                 MEDLINE=87165983; PubMed=3558397;
Medline=87165983; PubMed=3558397;
Morlort W., Villafranca J.B., Monzingo A.F., Ernst S.R., Katzin B.,
Rutenber B., Xuong N.H., Hamin R., Robertus J.D.;
"The three-dimensional structure of ricin at 2.8 A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
MEDLINE=96374222; PubMed=8780513;
MEDLINE=96374222; S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,
Molina-Svinth M.C., Robertus J.D.;
"Structure and activity of an active site substitution of ricin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97240820; PubMed=9086280;
Yan X., Hollis T., Svinth M., Day P., Monzingo A.F., Milne G.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
MEDLINE=25682010; Pubmed=7990130;
Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,
Pauptit R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure-based identification of a ricin inhibitor.";
J. Mol. Biol. 266:1043-1049(1997).
                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN. MEDLINE=91352005; PubMed=1881882; MEDLINE=91352005. Robertus J.D.; Robertus J.D.; Richard G. Ricin B-chain at 2.5-A resolution."; Proteins 10:260-269(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN
                                                                                                                                                                                                                  MEDLINE=91352004; PubMed=1881881;
Katzin B.J., Collins E.J., Robertus J.D.;
"Structure of ricin A-chain at 2.5 A.";
x-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                      Biol. Chem. 262:5398-5403(1987).
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SIMILARITY: Contains 2 ricin B-type lectin domains.
CAUTION: REF. 4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
DATABASE: NAME=Protein Spclight;
NOTE=Issue 31 of February 2003;
WWW="http://www.expasy.org/spotlight/articles/sptlt031.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00396; SHIGARICIN.
SMARY; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=CAR 000080.
N-LINKED [GLCNAC. . .) (IN MINOR FORM).
/FTId=CAR 000081.
N-LINKED [GLCNAC. . .).
N-LINKED [GLCNAC. . .).
E -> D [IN REF. 3).
A -> R [IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RICIN A CHAIN.
LINKER PEPTIDE.
RICIN B CHAIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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PDB; III.9; 16-JAN-02.
GlycoSuiteDB; P02879; -.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Ffam; PP00652; Ricin_B_lectin.
Pfam; PP00161; RIP; 1
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                                                                                                                                                                                EMBL, X03179; CAA26939.1; --
EMBL, X52908; CAA3095.1; --
EMBL, X0338; CAA26230.1; --
EMBL, A12892; CAA01058.1; --
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                                                                                                                                                                52 BLSNHABLLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 111
                                                                                                                                                                                                     96 ELSNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                                             156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                     36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRF1LV 95
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Bur. J. Blochem. 105.433-459(1980).

-! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.

-! SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN PAMILY. TYPE 2 RIP SUBFAMILY.

-! SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                2 IFPKQYPIINFTTAGATVOSYTNFIRAVRGRLT------VLPNRVGLPINORFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Agglutinin B chain].
Ricinus communis (Castor bean)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINES 6059449; PubMed=2999130; MEDLINES 66059449; PubMed=2999130; Roberts L.M., Lamb F.I., Pappin D.U.C., Lord J.M.; "The primary sequence of Ricinus communis agglutinin. Comparison with
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Araki T., Yoshioka Y., Funatsu G.; The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."; Biochim. Biophys. Acta 872:277-285 (1986).
                                           10;
Score 951; DB 1; Length 576;
Pred. No. 3.2e-80;
0; Mismatches 0; Indels
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Biol. Chem. 260:15682-15686(1985)
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MEDLINE=80178723; PubMed=6768555;
Lin T.T.-S., Li S.S.-L.;
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01-JAN-1988 (Rel. 06, Last seq
  97.9%;
                                         Matches 188; Conservative
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SEQUENCE OF 303-564.
TISSUE=Seed;
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Best Local Similarity
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P06750;
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EMBL; M12089; AAA33869.1; -. EMBL; S40368; AAB22584.1; -.

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85 ELSNHAELSVTLALDVINAYVVGCRAGNSAYFFHPDNQEDAEAITHLFTDVQNSFTFAFG 144
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                                                           InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00162; Ricin_B_lectin, 6.
Pfam; PF00161; RIP; II.
PRINTS; PR00196; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PSS0231; RICIN B_LECTIN; 2.
PROSITE; PSS0231; RICIN B_LECTIN; 2.
PROSITE; PSS0275; PRIGA_RICIN; 1.
PROSITE; PSS0275; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal
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SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
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N-LINKED (GLCNAC. ..).
F -> T (IN REF. 2).
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01-NOV-1990 (Rel. 16, Last sequence update)
15-5EP-2003 (Rel. 42, Last annotation update)
15-5EP-2003 (Rel. 42, Last annotation update)
15-5EP-2003 (Rel. 42, Last annotation update)
15-7EP-2003 (Rel. 43, Last annotation update)
15-7EP-2003 (Rel. 43, Last annotation precursor (RRNA N-glycosidase) (EC 3.2.2.22) (Alpha-TCS).
Trichosanthes kirilowii (Mongolian snake-gourd).
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R -> T (IN REF. 2).
F -> V (IN REF. 2).
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GlycoSuiteDB; P06750;
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"Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin.";

J. Biol. Chem. 265:8665-8669(1990).

[4]

SEQUENCE OF 24-270.

TISSUE-Tuberous root;

Wang Y., Olan R.O., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X., Tian G.Y., Ni C.Z.;

"Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application.";
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
NCBI_TaxID=3677;
                                                                                                                                                                                                       Chow T., Feldman R.A., Lovett M., Piatak M.,
"Isolation and DNA sequence of a gene encoding alpha-trichosanthin,
type I ribosome-inactivating protein.";
[3]
                                                                                   STRAIN=Maximowicz;
MEDLINE=91153657; PubMed=1999291;
Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
"Cloning of trichosanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X.-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
MEDLINE=94344957; PubMed=8066085;
Abou F., Pu Z., Chen M., Lin Y., Pan K.;
"Structure of trichosanthin at 1.88-A resolution.";
Proteins 19:4-13(1994).
                                                                                                                                                                                                                                                                                                               STRAIN=Maximowicz; TISSUE=Tuberous root; MEDLINE=90256789; PubMed=2341399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pure Appl. Chem. 58:789-798(1986).
                                                                                                                                                                                                      STRAIN=Maximowicz; TISSUE=Leaf;
MEDLINE=90256790; PubMed=2341400;
                                                                                                                                                              Gene 97:267-272(1991).
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InterPro; IPR001574; RIP.
PRAM; PP00161; FIP: 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
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| V -> VUNCHENNAYL (IN REF. 4).
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38.9%; Pred. No. 7.9e-24;
Live 42; Mismatches 49; Indels
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EMBL; M34858; AAA34207.1; -. EMBL; J05434; AAA34206.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Mood K.A., Lord J.M., Wawrzynzak E.J., Piatak M.;

Wood K.A., Lord J.M., Wawrzynzak E.J., Piatak M.;

"Preproabrin: genomic cloning, characterisation and the expression of the A-chain in Escherichia coli.";

Eur. J. Biochem. 198:723-732 (1991).

STYTHERSIS THROUGH THE ACTALYTIC INCCTIVATION OF 60S RIBOSOMAL STYLESIS THROUGH THE CATALYTIC INCCTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADRINE FROM POSITION 4,324 OF 28 SRNA. THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

CHICALLY CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.

CHICALLY THE B CHAIN IS COMPOSED OF TWO DOWAINS, EACH DOWAIN CONSISTS OF 3 HOWOLGOUS SUBDOMAINS, EACH DOWAIN.

CHICAL STRILLARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
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                                                           SVILALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFIDVQNRYTFAFGGNYDRLE 118
                                                                                                                      119 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-c precursor [Contains: Abrin-c A chain (rRNA N-glycosidase)
(EC 3.2.2.22); Abrin-c B chain].
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
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PROSITE; PS00275; SHIGA_RĪCIN; 1.
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InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF001652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP, I.
PRINTS; PR001396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 ERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYISN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97356562; PubMed=9212998; Mizukami H., Iida K., Kondo T., Golhara Y.; Mizukami H., Iida K., Kondo T., Golhara Y.; Mizukami H. at a parterial expression of a gene encoding ribosomeninactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 ODQVIKFTTEGATSQSYKQFİEALRQRLİTGGLIHDIPVLPDPTTVEERNRYİTVELSNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 QYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSNHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFGGNYDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         core eudicots; Rosidae;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
               BY SIMILARITY.

ABRIN C A CHAIN (BY SIMILARITY).

LINKER PEPTIDE (BY SIMILARITY).

ABRIN C B CHAIN (BY SIMILARITY).

RICIN B-TYPE LECTIN 1.

RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.7%; Score 327.5; DB 1; Length 562;
Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
(BY SIMILARITY).
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BY SIMILARITY.
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Ribosome-inactivating protein karasurin precursor (rRNA N-91ycosidase) (EC 3.2.2.22)
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                                                                                                                                                         62817 MW; 1FD0ABC7D7BA6278 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.1e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%; Preu. notive 22; Mismatches
                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                                    2-ALPHA.
2-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                               1-ALPHA.
                                                                                                                                                                    1-GAMMA.
                                                                                                                                                                                                                          2-GAMMA
                                                                                                                                                 1-BETA.
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Biol. Pharm. Bull. 20:711-713(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE OF 24-270.
MEDLINE=92005921; PubMed=1914000;
Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 43.99
Matches 82, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                     285
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435
462 AA;
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   Glycoprotein;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                               Chem. Pharm. Bull. 39:1244-1249(1991).
-!- FUNCTION: ABORITON-INDUCING PROTEIN. IT INACTIVATES EUKARXOTIC
-|- FUNCTION: SUBENITS.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  006077; P81374;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
(RC 3.2.2.2); Abrin-b B chain]
(RC 3.2.2.2); Abrin-b B chain]
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Agnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLIRSTLPGSQRYALIHLTNYADETIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specific adenosine on the 28S FRMA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Gaps
                                                                                                                                                                                                                                                                                                                                           PIR; JC5606; JC5606.
PIR; JU0393; JU0393.
HSSP: P09999; JIMG.
InterPro; IPR001574; RIP.
PFfam; PF00161; RIP; 1.
PRINTS; PR00395; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN, 1.
PROSITE; PS00275; SHIGARICIN, 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                    "The complete amino acid sequence of an abortifacient protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.6%; Score 326; DB 1; Length 289; 39.6%; Pred. No. 6.6e-23;
Poyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REMOVED IN MATURE FORM.
BY SIMILARITY.
883D3E3242887E26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KARASURIN-C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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24 270 KA
271 289 RE
183 183 BY
289 AA; 31704 MW;
                                                                                                                                                                                                                                                                                                                                EMBL; AB000666; BAA21786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72; Conservative
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270
270
289
183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxin, Signal
                                  karasurin."
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SEQUENCE
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                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific adenosine on the 28S frnA.
--- SUBUNIT: DISULFIDE-LINKED DIMER OF AND B CHAINS.
--- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGUS SUBDOMAINS (ALPHA, BETA, GAMMA).
--- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
--- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                        MEDLINE=93169023; PubMed=7763422;
Kimura M., Sumizawa T., Funatsu G.;
The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic proteins from the seeds of Abrus precatorius.";
Biosci. Biotechnol. Biochem. 57:166-169(1993).
-!- FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CAPALYTIC INACTIVATION OF 60S RIBOSOWAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S. RNA. ABRIN-A IS MORE TOXIC THAN RICIN.
-!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
            Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
"Primary structure of three distinct isoabrins determined by cDNA
sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N -> D (IN REF. 2).
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BY SIMILARITY.

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PYRROLLDONE CARBOXYLIC ACID (BY
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BY SIMILARITY.
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RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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2-BETA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S32430; S32430.
HSSP; P11140; JABR.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 - GAMMA
MEDLINE=93132798; PubMed=8421313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00652; Ricin B lectin; 6. Pfam; PF00161; RIP; 1.
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                                                                                 SEQUENCE OF 260-527.
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452
469
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416
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MOD_RES
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58 ELSVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 117
                                                                                                                                                                                                                                                                                                           61 TESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYIDL 116
                                                                                                                                                                                                                                                                                                                                     118 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
                                                                                                                                                                                                                                                             1 ODQVIKFTTEGATSQSYKQFIEALRQRLTGGLIHGIPVLPDPTTLQERNKYISVELSNSD 60
                                                                                                                                                                                                                                    ----VLPNRVGLPINQRFILVELSNHA
                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                              16;
                                                                                                                                                                                     ; DB 1; Length 527; 2.6e-22;
                                                                                                                                                                                                             69; Indels
D -> N (IN REF. 2).

AE -> PQ (IN REF. 2).

E -> N (IN REF. 2).

Y -> D (IN REF. 2).

Y -> D (IN REF. 2).

R -> K (IN REF. 2).

N -> S (IN REF. 2).

N -> S (IN REF. 2).

N -> S (IN REF. 2).

R -> K (IN REF. 2).

R -> G (IN REF. 2).

R -> G (IN REF. 2).

E -> Q (IN REF. 2).

H -> T (IN REF. 2).

H -> T (IN REF. 2).

H -> T (IN REF. 2).

H -> T (IN REF. 2).

H -> T (IN REF. 2).
                                                                                                                                                                                                            21; Mismatches
                                                                                                                                                                                     Score 323;
Pred. No. 2
                                                                                                                                                                                                                                      6 QYPIINFTTAGATVQSYTNFIRAVRGRLT--
                                                                                                                                                              59114 MW;
                                                                                                                                                                                   33.3%;
                                                                                                                                                                                                             83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           173 RVGVSIRIN 181
                                                                                                                                                            527 AA;
                                                                                                                                                                                     Query Match
Best Local Similarity
   2291
3350
3378
3426
4431
4484
4491
5002
513
                         CONFLICT
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin II precursor (FRNA glycosidase) (EG 3.2.2.22) (BD2). 282 AA. PRT; STANDARD; RIP2 BRYDI P98184, Q9S8J0, 16-OCT-2001 (Rel NCBI_TaxID=3652;

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Cucurbitales, Cucurbitaceae, Bryonia. SEQUENCE FROM N.A.

Siegall C.B., Gawlak S.L., Marquardt H., "Bryodin 2 a ribosome-inactivating protein isolated from the plant Patent number US5597569, 28-JAN-1997 Bryonia dioica."

Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B., MEDLINE=95151812; PubMed=7849072; SEQUENCE OF 22-42. TISSUE=Root;

"Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive immunoconjugates."; Marquardt H.;

Bioconj. Chem. 5:423-429(1994).
-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at on specific adenosine on the 28S FRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY: TYPE 1 RIP SUBFAMILY:

nigra L."; Plant Mol. Biol. 22:1181-1186(1993). -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN

between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). SWISS-PROT entry is copyright. It is produced through a collaboration 7; 84 TVALDVVNVÝVVAYRAGNTAÝFL---ADASTEANNVLFAGI-NHVRLPYGGNÝDGLETAA 139 62 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 121 83 24 INFSLIGATGATYKTFIRNLRTKÍTVGTPRVYDIPVLRNAAAGLARFQLÝTLTNYNGESV RIBOSOME-INACTIVATING PROTEIN BRYODIN II ----RFILVELSNHAELSV 122 GNL-RENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAARFQYIE 176 33.0%; Score 320.5; DB 1; Length 282; 46.0%; Pred. No. 2.1e-22; tive 24; Mismatches 54; Indels 17; Gaps (POTENTIAL) InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR001036; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN: 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; BY SIMILARITY.
N-LINKED (GLCNAC. . .) (PC
; C52BE2F6A873769C CRC64; 10 INFTTAGATVQSYTNFIRAVRGRLTV-LPNRVGLPINQ---Multigene family; Glycoprotein; Signal. EMBL; I34238; -; NOT_ANNOTATED_CDS. HSSP; P09989; 1MRJ. 183 183 B 25 25 N 282 AA; 30754 MW; 81; Conservative Local Similarity P09989 ACT SITE CARBOHYD SEQUENCE Query Match SIGNAL This Matches SOUTH THE WAY WAY THE FEE SO à 임 à g à d

MEDLINE=96215449; PubMed=8647092;
Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
"Characterization and molecular cloning of Sambucus nigra agglutinin V
(nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra)."; 01-0CT-1993 (Rel. 27, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
38-FBB-2003 (Rel. 41, Last annotation by Gontains: Nigrin b A chain (RNA N-glycosidase) (EC 3.2.2.2); Nigrin b B chain]
28-BNATOCLS (Propean elder)
28-KRATOCLS (Propean elder)
28-KRATOCLS (Propean elder)
28-KRATOCLS (Propean elder)
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38-KRATOCLS (PROPEAN ELGRATOCLS EQUENCE OF 26-49 AND 298-321.

RX. MEDLINE=9400307; PubMed=8400135;

RA. MIDCARE T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,

"Isolation and partial characterization of nigrin b, a non-toxic

RT. "Isolation and partial characterization of nigrin b, a non-toxic

RT. novel type 2 ribosome-inactivating protein from the bark of Sambucus

RT. nigra L.",

Plant Mol. Biol. 22:1181-1186(1993).

CC. -! FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN 563 A.A. Eur. J. Biochem. 237:505-513(1996). PRT; STANDARD: P33183; P33184; P93542; SEQUENCE FROM N.A. NCBI_TaxID=4202; NIGB SAMNI

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NCBI_TaxID=3652;
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                                                                                                                                                          CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
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PROSITE; PS00275; SHIGA RICIN; 1.
PROSITE; PS50231; RICIN_B LECTIN; 2.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.
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SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN
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              SYNTHESIS. THE A CHAIN IS RESPONDEDE FOR INHIBITING PROTEIN SYNTHESIS. THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITES BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S.RNA. B. CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT PACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
                                                                                                                                                                             specific adenosine on the 28S rRNA.
SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBPAMILY.
SIMILARITY: Contains 2 ricin B-type lectin domains.
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38.4%; Pred. No. 7.6e-21;
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---SVARSLLVVIQMVSEAARFRY 194
                                                                                                                                    Bioconj. Čhem. 5:423-429(1994).
-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
-!- PROTEIN SYNTHESIS IN ANIMAL CELLS.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- BIOTECHNOLOGY: Especially useful as immunotoxin for pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specific adenosine on the 28S TRNA.
-!- PIM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL PRODUCE A SHORTER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of ribosome-inactivating proteins isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning and expression of a gene encoding bryodin 1 from Bryonia
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97228081; PubMed-9115985;
Gawlak S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "N-Lerminal sequence of some ribosome-inactivating proteins."; Int. J. Pept. Protein Res. 33:263-267(1989).
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bryonia dioica and their utility as carcinoma-reactive
142 DNLETAANTRRESIELGPSPLDGAITSLYHGD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent number US5541110, 30-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89326691; PubMed=2753596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bryonia dioica.";
Biochemistry 36:3095-3103(1997).
                                175 IEGEMRTRIR 184
                                                               195 İEQEVRRSLQ 204
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142 GKIRENIPLGLPALDSAITTLYYYTAS-----SAASALLVLIQSTAESARYKFIEQQIGK 196 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181

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RIBOSOME-INACTIVATING PROTEIN BRYODIN I. MISSING IN MATURE PROTEIN. BY SIMILARITY.
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35.7%; Pred. No. 5.8e-21;
iive 45; Mismatches 56; Indels 16; Gaps
                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
E-K. REDUCES ACTIVITY 10-FOLD.
RSSIS -> LRHXI (IN REF. 3).
                                                PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 31788 MW; E966CD9C031A42DB CRC64;
                                                                     Multigene family; Glycoprotein; Signal
an email to license@isb-sib.ch)
            EMBL; 124020; -; NOT_ANNOTATED_CDS.
PIR; S16491; S16491.
                           PDB; 1BRY; 04-MAR-98.
InterPro; 1PR001574; RIP.
Pfam; PF00161; RIP; 1.
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270
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63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 121

62

INFTTAGATVOSYTNFIRAVRGRLTVLPNRVGLPI-----NORFILVELSNHAELSVT 25 VSFRLSGATTTSYGVFIKNURBALPYERKVYNIPLIRSSISGSGRYTLLHLTNYADETIS

65; Conservative

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Local Similarity

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MEDLINE=95333188; PubMed=7608980;
A Tahirov T.H., Lu T.-H., Lidaw Y.-C., Chen Y.-L., Lin J.-Y.;
Tahirov T.H., Lu T.-H., Lidaw Y.-C., Chen Y.-L., Lin J.-Y.;
Tahirov T.H., Lu T.-H., Lidaw Y.-C., Chen Y.-L., Lin J.-Y.;

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin-a at 2.14 A.";

"Crystal structure of abrin of 608 RIBOSONAL STRUCTION: THE B CALININ ERON POSITION 0F 608 RIBOSONAL STRUCTION: THE B CALININ IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITARES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT FACILITARES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PROCEEDES ENDOCYTOSIS.

-I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 288 FRNA.

-I- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMALNS (ALPHA, BETA, GAAMA).
      P11140, P2889;
01-JUL-1989 (Rel. 11, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Abrin-a precursor [Contains: Abrin-a A chain (rRNA N-glycosidase)
(EC 3.2.2.22); Abrin-a B chain]
Abrus precatorius (Indian licorice) (Crab's eye)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;
"The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from the seeds of Abrus precatorius.";
Agric. Biol. Chem. 52:1095-1097(1988).
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=93132798; PubMed=8421313;

Hung C.-H, Lee M.-C., Lee T.C., Lin J.-Y.;

"Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.";

J. Mol. Biol. 229:263-267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evensen G., Mathiesen A., Sundan A., "Direct molecular cloning and expression of two distinct abrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEDLINE=92371656; PubMed=1505674;
MEDLINE=92371656; PubMed=1505674;
MEDLINE=1., Chow L.-P., Tsugita A., Lin J.-Y.;
"The complete primary structure of abrin-a B chain.
FRBS Lett. 309:115-118(1992).
528 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. Chem. 266:6848-6852(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91201329; PubMed=2016300;
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  STANDARD;
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DR Farry: PR00157; RIP; I.

DR SMART; SM00458; RICIN, 2.

PR05ITE; P800275; RICIN, 2.

PR05ITE; P800275; RICIN, 2.

PR05ITE; P800275; RICIN, 3D-structure; Prrorolidone carboxylic acid.

ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense; Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense Hydrolase; Prorein synthesis inhibitor; Toxin; Repeat,

"ant defense Hydrolase; Prorein synthesis inhibitor; Tox
                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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INTERCHAIN (BY SIMILARITY).
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PYROLIDONE CARBOXYLIC ACID.
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M-LINKED (GLCNAC. . .).
M-LINKED (GLCNAC. . .).
M-SING (IN REF. 4).
N -> Y (IN REF. 4).
T -> P (IN REF. 4).
T -> P (IN REF. 4).
  INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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31.3%; Score 303.5; DB 1; Length 528; 41.1%; Pred. No. 1.6e-20; tive 26; Mismatches 64; Indels 19;
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Matches 76; Conservative
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RESULT 13
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                                62 TLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFIDVQNRYTFAFGGNYDRLEQ 119
                                                                               120 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 179
                                                                                                       119 WAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRV 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 INFTTAGATVQSYTNFIRAVRGRL------TVLPNRVGLPINQRFILVELSNHAEL 59
          64
                                                                                                                                                                                                                                                                                                                                                                                                                Islam M.R., Hirayama H., Funatsu G.,

"Complete amino acid sequence of luffin-b, a ribosome-inactivating
protein trons spong gourd (Luffa cylindrica) seeds.";

Agric. Biol. Chem. 55:229-28(1991).

-! CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.

-! SIMILARITY: BLOONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                      (EC 3.2.2.22).
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Elukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|: :|| :||: || ||:||:
3 VSFSLSGADSKSYSKFITALRXALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK
                                                       65 EVGIDVINAYVVAYRAGIQSYFLRDAPSSASD----YLFIGT-DOHSLPFYGTYGDLER
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InterPro; IPR001574; RIP.
Pram; PP00161; RIP; 1.
PROPINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antivixal; Protein synthesis inhibitor; Hydrolase;
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                                                                                                                                                                                                                                                     01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Yamada T., Ohki S.T., Osaki T.;

Yamada T., Ohki S.T., Osaki T.;

"Cloning and analysis of a cDNA coding a putative ribosome-
inactivating protein from Cucumis figarei.";

Plant Biotechnol. 17:337-340(2000)

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S rRNA.

-!- SIMILARITY: BELOWGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI------NQRFILVELSNHAELSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 VKFSLLGSNHKSYSKFITSMRNALPNAGDIYNIPLLVPSISGSRRYILMQLSNYEGNTIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 MAVDVTNVYIMGYLVNGTSYFF---NETDAQLASKFVFQGTKSITLPYSGNYQKLQSVAR
                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                      Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
PUTATIVE RIBOSOME-INACTIVATING PROTEIN.
BY SIMILARITY.
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00161; RIP, 1.

BRNTS, PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN; 1.
Plant defense; AntivixaI; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4EFD4966E604DA41 CRC64;
                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Mismatches
  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31771 MW;
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InterPro; IPR001574; RIP.
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  STANDARD;
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286
185
103
110
252
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103
110
252
286 AA;
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                                                                                                                                                                                          Cucumis figarei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxin; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
RIP1 CUCFI
Q9FRX4;
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CARBOHYD
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us-10-083-336a-6.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 KAITVÄVDVTNVYIMGYLVNSTSYFF---NESDÄKLASQYVFKGSTIVTLPYSGNYEKLQ 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
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                                                                                                                                                                                                                                                                                                                                                      inactivating protein from Luffa cylindrica.",
Plant Mol. Biol. 18:1199-1202(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 INFITAGATVQSYTNFIRAVRGRLTVLPNRVGLPIN------QRFILVELSNHAE
                                                                                                                                      N-grycosidase) (EC 5.2.2.2.2).
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Luffa cylindrica (Smooth loofah) (Sponge gourd).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae, Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         specific adenosine on the 28S rRNA.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIBOSOME-INACTIVATING PROTEIN LUFFIN-
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PRINTS, PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                  Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.;
"Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 277;
                                                 01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
08-ERB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-alpha precursor (rRNA N-glycosidase) (EC 3.2.22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28.3%; Score 274.5; DB 1; Lengtu 23.3%; Pred. No. 3.66-18; Mells Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EA17FC27998C25AC CRC64;
                 277 AA.
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                 PRT;
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                                                                                                                                                                                                                                                                                              MEDLINE=92288316; PubMed=1600156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X62371; CAA44229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P16094; 1AHC.
InterPro; IPR001574; RIP.
                 STANDARD;
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190 IIERISKNQ 198
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Best Local Similarity
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                         NCBI_TaxID=3670;
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                 RIPA LUFCY
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SEQUENCE
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RIPA LUFCY
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286 AA.

PRT;

STANDARD;

RIPI MOMCH ID RIPI MOMCH

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-!- CARTALYITC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
             01-APR-1990 (Rel. 14, Created)
01-AMR-1990 (Rel. 21, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein momoratin I precursor (rRNA Momoradase) (BC 3.2.2.2) (Alpha-momorcharin) (Alpha-MMC)
N-glycosidase) (BC 3.2.2.2) (Alpha-momorcharin) (Alpha-MMC)
Momoradac charantia (Bitter gourd) (Balsam pear).
Bukaryota, Viridiplantes, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                            MEDLINE=91159486; PubMed=2001404;
Ho W.K.K., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;
"Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Casellas P., Dussossoy D., Falasca A.I., Barbieri L., Guillemot J.C., Ferrara P., Bolognesi A., Cenini P., Stirpe F.; "Trichokirin, a ribosome-inactivating protein from the seeds of Trichosanthes kirilowii Maximowicz. Purification, partial characterization and use for preparation of immunotoxins."; Eur. J. Biochem. 176:581-588(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          depurinating mechanism of two ribosome-inactivating proteins."; Biochem. J. 309:285-298(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=94356447; PubMed=8075985;
Ren J., Wang Y., Dong Y., Stuart D.I.;
The N-glycosidase mechanism of ribosome-inactivating proteins implied by crystal structures of alpha-momorcharin.";
Structure 2:7-16(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94192822; PubMed=8143869;
Husain J., Tickle I.J., Wood S.P.;
"Crystal structure of momordin, a type I ribosome inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nrterminal sequence of some ribosome-inactivating proteins.";
Int. J. Pept. Protein Res. 33:263-267(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Studies on crystal structures, active-centre geometry and
                                                                                                                                                                             eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein from the seeds of Momordica charantia.";
FEBS Lett. 342:154-158(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95344383; PubMed=7619070;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1088:311-314(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.16 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89326691; PubMed=2753596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Seed;
MEDLINE=89005108; PubMed=3262509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X57682; CAA40869.1; -. PIR; S14273; RLPUGG.
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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P16094; P24697;
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                                                                                                                                                                                                                                                                                                                                                            protein
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GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT
                                                                                                                                                                                                                                                                                                                                                                                                        Length 286;
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                                                                                                                                                                                                                                                                                                                                                                                          3B89FF1AE6B25986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       28.0%; Score 272; DB 1; 34.2%; Pred. No. 6.3e-18;
                                                                                     1-DEC-1992 (Rel. 24, Created)
1-DEC-1992 (Rel. 24, Last sequence update)
5-SEP-2003 (Rel. 42, Last annotation update)
                                                                          286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               ; Pred. No. 6.3e 39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
                                                                        PRT;
                                                                                                                                                                           MEDLINE=93027170; PubMed=1408771;
                                                                                                                                                                                                                                                                                                                                                                                          32031 MW;
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PIR; Z25560; Z25560.
PDB; 1CF5; 07-UTN-99.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                     63; Conservative
                                                                         STANDARD;
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286
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                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=3672;
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                           R 182
                                        R 197
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                                                                                      01-DEC-1992
01-DEC-1992
                                                                                                                                                                       TISSUE=Seed
                                                                         MOMBA
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SEQUENCE
                           182
                                        197
 122
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                                                                                P29339
                                                           RESULT 15
RIP2 MOMBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT
                                                                 PRINTS; PR00396; SHIGARICIN.
PROSITE; PR00275; SHIGA RICIN; 1.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal; Glycoprotein; 3D-structure.
SIGNAL 1 23
                                                                                                         RIBOSOME-INACTIVATING PROTEIN MOMORDIN I. MISSING IN MATURE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    28.1%; Score 273; DB 1; Length 286; 34.8%; Pred. No. 5.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                       31532 MW; E1B013ABEBC216CF CRC64;
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/FTId=CAR_000082.
                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Conservative
                                                    GlycoSuiteDB; P16094; -.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
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183
250
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259
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286 AA;
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142 GKPREKIPIGLPALDSAISTLHYDS----TAAAGALLVIIQTTAEAARFKYIEQQIQE 196
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LALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAG 122
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"Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologome inactivating proteins.";
Nucleic Acids Res. 20:4662-4662(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
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:::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::| | :::
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Momordica balsamina (Bitter gourd) (Balsam pear).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
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PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; Signal;
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141 KIRENIDLGLPALSSAITTLFYYNA----QSAPSALLVLIQTTAEAARFKYIERHVAKY 195 ДQ

183 IRYN 186

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Search completed: February 10, 2004, 16:23:24 Job time : 7.30467 secs

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February 10, 2004, 16:17:00 ; Search time 25.2187 Seconds (without alignments) 1933.961 Million cell updates/sec
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971
1 MIFPKQYPIINFTTAGATVO......ARFQYIEGEMRTRIRYNRRS 189
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q41174 ricinus com Q94bw3 cinnamomum Q94bw4 cinnamomum			
SUMMARIES ID	Q41174 Q94BW3 Q94BW4	Q94BW5 Q9FV22 Q9FK84	041216 004367 09LRE3 09AVR2	Q06076 Q8LPV7 Q38760 Q94522 Q8GT32 Q41611
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% Query Match	97.9 38.6	38.2	4 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9	32.8 32.6 32.0 31.7 31.7
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17 303.5 31.3 252 10 Q38761 18 302 31.1 565 10 Q04071 19 303.5 30.7 547 10 Q00852 20 294.5 30.7 547 10 Q00852 21 297.5 30.6 251 10 Q06235 22 296.5 30.5 251 10 Q06235 23 296.5 30.5 251 10 Q06235 24 296.5 30.5 251 10 Q06235 25 273 281 270 0 Q41358 26 273 281 570 0 Q41358 27 27.1 28.1 570 0 Q41257 28 270 27.8 289 10 Q04025 29 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 270 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 27.8 289 10 Q04025 20 270 270 270 270 20 270 270 270 270 20 270 270 270 270 20 270 270 270 270 20 270 270 270 270 20 270 270 270 270 20 20 20 20 20 20 20 20	Q38761 abrus preca 004071 sambucus ni 000800 luffa cylin Q9m6e9 abrus preca 096237 abrus preca 004072 sambucus ni 096235 abrus preca 004072 sambucus ni 086235 abrus preca 094158 sambucus ni 081845 viscum albu 091845 viscum albu 081846 viscum albu 081846 viscum albu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081846 viscum albu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081845 jatropha cu 081846 viscum albu 081845 gatrostemma 081846 gynostemma 081846 gynostemma	GNMENTS 541 AA. d) equence update) nnotation update)	tophyta; Embryophyta; Tracheophyta; udicotyledons; core eudicots; Rosidae; rbiaceae; Ricinus. d J.M.; d J.M.; 992). RODYSIS OF THE N-GLYCOSIDIC BOND AT ONE 8S RRMA. RIBOSOME-INACTIVATING PROTEIN FAMILY. ctin. in. 6. N; 2. 11. 2; 1.
17 303.5 31.3 252 10 18 300.5 30.9 278 10 20 298.5 30.9 278 10 22 296.5 30.6 251 10 23 295.5 30.6 251 10 24 296.5 30.6 251 10 25 27 273 28.1 264 10 26 27 273 28.1 264 10 27 271 27.9 286 10 28 27 271 27.9 286 10 30 267 27.8 286 10 31 266.5 27.4 604 10 32 26.5 27.4 604 10 32 26.5 27.4 266 10 34 26.5 27.4 266 10 35 26.5 27.4 269 10 36 25.9 26.7 251 10 37 25.9 26.7 251 10 38 25.3 26.1 531 10 39 25.3 26.1 531 10 31 266.5 27.4 268 10 32 25.2 27.4 203 10 34 26.5 27.4 269 10 35 25.9 26.7 259 10 36 25.9 26.7 259 10 37 25.9 26.7 259 10 38 25.3 26.1 531 10 39 25.3 26.1 531 10 41 247 25.4 293 10 42 246.5 25.4 203 10 44 246.5 25.4 203 10 45 246.5 25.4 203 10 47 1.NOV-1996 (TrEMBLrel. 23, 10 48 246.5 25.4 203 10 49 241.74 DT 01-NOV-1996 (TrEMBLrel. 23, 10 49 245.5 25.4 203 10 41 247 25.4 203 10 42 246.5 25.4 203 10 44 246.5 25.4 203 10 45 246.5 25.4 203 10 46 241.74 DT 01-NOV-1996 (TrEMBLrel. 23, 10 48 246.5 25.4 203 10 49 246.5 25.4 203 10 41 247 25.4 203 10 45 246.5 25.4 203 10 46 241.74 DT 01-NOV-1996 (TrEMBLrel. 23, 10 48 246.5 25.4 203 10 49 246.5 25.4 203 10 40 10 10 10 10 10 10 10 10 10 41 247 25.4 203 10 42 246.5 25.4 203 10 44 246.5 25.4 203 10 45 246.5 25.4 203 10 46 245.5 25.4 203 10 47 10 10 10 10 10 10 10 10 10 10 10 10 10	Q38761 004071 000980 Q906E3 Q96237 006235 Q96237 Q975H2 Q975H2 Q915KQ5 Q916544 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q916544 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q916544 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q91654 Q9165	ALIGNMENTS PRT; 541 Created) Last sequence Last annotati 2) (rRNA N-gl)	reptophyl; reptophyl; reudicol phorbiace 3311; Cord J.M 7(1992). 7(1992). 7(1992). 17(1992). 17(1992). 17(1992). 17(1992). 17(1992). 17(1992). 17(1992). 17(1992). 17(1992). 17(1992). 17(1992). 17(1992). 17(1992).
17 303.5 31.3 252 18 302 31.1 565 19 300.5 30.9 278 20 296.5 30.9 278 22 296.5 30.6 251 23 296.5 30.6 251 24 290.5 30.6 251 25 296.5 30.5 256 24 290.5 29.9 251 25 273 28.1 264 27 271 27.9 284 28 270 27.8 289 39 257 27.1 565 31 266.5 27.4 604 32 26.5 27.4 604 32 26.5 27.4 604 32 26.5 27.4 604 32 26.5 27.4 604 32 26.7 27.8 289 40 26.7 27.8 289 41 247 25.4 293 42 26.7 259 44 246.5 27.4 604 32 26.7 259 44 246.5 25.4 293 45 246.5 27.4 604 37 259 26.7 259 48 246.5 27.4 604 38 26.8 27.3 603 44 246.5 25.4 293 45 245.5 25.4 293 46 247 25.4 293 47 246.5 25.4 293 48 246.5 25.4 298 49 247 25.4 293 40 24174, PRELIMINARY; 41 247 25.4 293 42 247 25.4 293 43 246.5 25.4 293 44 246.5 25.4 293 45 245.5 25.4 293 46 247 25.4 293 47 246.5 25.4 293 48 246.5 25.4 293 48 246.5 25.4 293 48 246.5 25.4 293 49 246.5 25.4 293 49 246.5 25.4 293 40 241174, PRELIMINARY; 41 247 25.4 293 42 246.5 25.4 293 43 246.5 25.4 293 44 246.5 25.4 293 45 245.5 25.4 293 46 245.5 25.4 293 47 246.5 25.4 293 48 246.5 25.4 293 49 247 40 1.NOV-1996 (TEMBLIPLE) 48 PROFITE; PROOUTE; PROOUTER; PROO		01, 001, 123, 13, 123, 123, 123, 123, 123, 123	bean 'Strain'
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                                                                                                                                                                           61 ELSNHAELSVTLALDVTNAXVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                         GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 171
                                                                                                                                                                                                                                                              121 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 YPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSN-H 56
                                                                         -----VLPNRVGLPINQRFILV 51
                                                                                                            1 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patterns.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
genes encoding cinnamomin proteins and study of their expression
                                      10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIFIC ADENOSINE ON THE 28S RRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL. ANOBORS; ARRS460.1;

-InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Lauraceae, Cinnamomum.
NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
17pe 2 ribosome-inactivating protein cinnamomin III precursor
(EC 3.2.2.2) (rRNA N-91ycosidase).
   Length 541;
                                        0; Indels
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 97.9%; Score 951; DB 10;
94.9%; Pred. No. 2.8e-82;
live 0; Mismatches 0;
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48.1%; Pred. No. 3.7e-27;
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                                                                           2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
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SMART; SMOR4S9; RICIN; 2.
PROSITE; PS50231; RICIN B.LECTIN; 2.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                   172 FQYIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                      181 FOYIEGEMRTRIRYNRRS 198
                                      Matches 188; Conservative
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Query Match
Best Local Similarity
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hes 90; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 LEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33 YQTVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMRDGSTVPDSKRFILVELSNWA 92
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDDSLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AX039002; AAK035591; -.
InterPro; IPR000772; Ricin_B_lectin.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Yang O., Gong Z.Z., Liu W.Y.; Yang O., Gong Z.Z., Liu W.Y.; Wolecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI------NQRFILVELSN-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 47.6%; Pred. No. 5.8e-27; noservative 27; Mismatches 56; Indels 15; Gaps
                                                                                                                                                                                                                                                 Cinnamomum camphora (Camphor tree).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 580;
                                                                                                                                                                                                             Type 2 ribosome-inactivating protein cinnamomin II precursor (EC 3.2.2.22) (rRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1-DRC-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin I precursor (EC 3.2.2.22) (rRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CINNAMOMIN II.
37E4289ECCE0CBFF CRC64;
                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                         580 AA.
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47.6%; Pred. No. 5.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00396; SHIGARICIN.
SMART; SMOAFS, RICIN; 2.
PROSITE; PS5021; RICIN; 2.
Hydrolase; Signal; Toxin.
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                                 208 YRVRESI 214
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177 GEMRTRI 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 LEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 YQTVTFTTXXATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xie L., Liu W.-Y., Wang E.-D.;
"Molecular cloning of cinnamomin A-, B-chain and the expression,
molecular cloning of cinnamomin A-, B-chain and the expression,
purification, characterization and mutagenesis of the A-Chain.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF255548; AAF68978.2; --
HSSP; P02879; 2AAI.
                                                                                                                                        Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AV039801, AAK82458.1; —InterPro, IPR000772; Ricin B_lectin.
InterPro, IPR001574; RIP.
                                                                                   Yang Q., Gong Z.Z., Liu W.Y.; "Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 YPIINFTTAGATVOSYTNFIRAVRGRLT-----VLPNRVGLPINORFILVELSN-H
                                                                                                                                                                                                                                                                                                                                                                                                                                57; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (rRNA
Cinnamomum camphora (Camphor tree).

Wakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Laurales; Lauraceae, Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cinnámomum camphora (Camphor tree).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
                                                                                                                                                                                                                                                                                                                                             TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 370.5; DB 10; Length 581;
; Pred. No. 9e-27;
25; Mismatches 57; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                         GERFSFBRFBA3D196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      549 AA.
                                                                                                                                                                                                                                                                                                                                                            CINNAMOMIN I
                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                  PROSITE, PS50231; RICIN B LECTIN; 2. Hydrolase; Signal; Toxin.
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                                                                                                                                                                                                                                            Pfam, PF00652; Ricin B lectin; 5. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                           581 AA; 64215 MW;
                                                                  SEQUENCE FROM N.A. Yang Q., Gong Z.Z., Liu W.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                      38.2%;
                                                                                                                                                                                                                                                                       PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-glycosidase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 YRVRGSI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 GEMRTRI 183
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                              33
                                                                                                                                patterns.";
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYTD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 LEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yuan H., Wang L., Wang Y., An C., Chen Z.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YQTVTFTTKKATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWA
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                                                                                                                                                                                                                                                                                                                                                                                                           7 YPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVELSN-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trichosanthes kirilowii (Mongolian snake-gourd).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Trichosanthes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AF367252, AAK52960.1; -.
                                                                                                                                                                                                                                                                                                       DB 10; Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.4%; Score 334; DB 10; Length 289; Best Local Similarity 38.9%; Pred. No. 1.1e-23; Matches 72; Conservative 42; Mismatches 49; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.0%; Score 368.5; DB 10; Length 48.1%; Pred. No. 1.3e-26; tive 25; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 AA; 31706 MW; A6D5602549CA5657 CRC64;
                                                                                                                                                                                                                                              549 AA; 60648 MW; 02607FE607CA44B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 AA.
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InterPro; IPR000772; Ricin_B_lectin.
                                                                                                       PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00161; RIP, 1.
SRINTS, PR00396; SHIGARICIN.
PROSITE, PS00275; SHIGARICIN; 1.
HydroLase; Signal; Toxin.
                      InterPro, IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                           90; Conservative
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                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GEMRTRI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 YRVRGSI 182
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                                                                                                                                                                                             Hydrolase; Toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFQYIEGE 178
                                             119 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 178
                                                                     60 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 IISVAIDVTNVYIMGYRAGDISYFF---NEASAIEAAKYVFKDSMRKITLPYSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 VSFRLSGAISSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSQRYALVHLINYADE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I Chuan Hsueh Pao 21.42-51(1994).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 INFTTAGATVQSYTNFIRAVRGRLTVLPN-------RVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids 1, Cucurbitales, Cucurbitaceae, Trichosanthes.
NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zheng H., Wang B., Shaw P., Yeung H.; "[Cloning and DNA sequencing of the gene encoding trichosanthin].";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.2%; Score 332; DB 10; Length 289; 38.9%; Pred. No. 1.7e-23; tive 42; Mismatches 49; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosome inactivating protein precursor (EC 3.2.2.22) (FRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 AA; 31650 MW; 286AC14D48BCA175 CRC64;
                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Trichosanthin (EC 3.2.2.22) (rRNA N-glycosidase). TRICHOSANTHIN, TCS.
TRICHOSANTHIN, TCS.
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                                                                                                                                                                                                                                                                                                  289 AA.
                                                                                                                                                                                                                                                                                                                                              Created)
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PRINTS, PR00396, SHIGARICIN.
PROSITE, PS00275, SHIGA_RICIN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; S70176; AAB31048.1; -. HSSP; P09989; 1MRJ.
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                                                                                                                                    179 MRTRI 183
                                                                                                                                                                               194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                           Q41216
Q41216;
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004367
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Q41216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; Plant J. 12:1251-1260(1997).
--- CATALYIIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
--- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh; "Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi)."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 YPIINFTTAGATVQSYTNFIRAVR-----GRLTVLPNRVGLPINQRFILVELSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 YPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFVLVLLTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI - - THLFTDVQNRYTFAFGGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 DNLETAAGTRRESIELGPSPLDGAITSLYYDE-----SVARSLLVVIQMVSEAARFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
RIBOSOME INACTIVATING PROTEIN, A CHAIN.
RIBOSOME INACTIVATING PROTEIN, B CHAIN.
              Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trichosanthes sp. Bac Kan 8-98.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 563;
                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=98112023; PubMed=9450339;
Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichobakin (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3ED2B6C08E796205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.9%; Score 329.5; DB 1 40.5%; Pred. No. 7.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00396; SHIGARICIN.
SMART; SW00458; RICIN; 2.
PR0SITE; PS50231; RICIN B LECTIN; 2.
PR0SITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00652; Ricin B lectin; 6. Pfam; PF00161; RIP; 1.
Sambucus nigra (European elder)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563 AA; 62336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U76524; AAC15886.1; -. HSSP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 IEGEMRTRIR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 İEQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297
563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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62694 MW; 8261681A6DB55CB8 CRC64;

564 AA;

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SEQUENCE
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                                                                                                                                                                                                                                                                                        62 VAIDVINVYVMGYRAGDISYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQIAA 118
                                                                                                                                                                                                                                                                                                                                       63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-BAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                                                                                                         GNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
                                                                                                                                                                                                                        10 INFITAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 62
                                                                                                                                                                                                                                        2 VSPRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS 61
-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RENA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMB1, AB039324; BAA92530.1; -.
HINCEPPO: P09989; INKJ.
INTERPO: IRROLIS'4; RIP.
PEAN; PROJ161; RIP.
PROSTIE: PS00161; RIP.
PROSTIE: PS00275; SHIGALIGN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;
"Molecular cloning of ebulin l.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYIC ACTIVITY: ENDOHYPROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RENA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, A4400822; CAC33178.1; -.
                                                                                                                                                                                                     16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                         33.6%; Score 326; DB 10; Length 247; 39.6%; Pred. No. 5e-23; Live 44; Mismatches 50; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA N-glycosidase).
                                                                                                                                   247 247 27199 MW; 89811AC32892F03F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EBULIN L A-CHAIN.
EBULIN L B-CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMAKT; SMUU450; ALLAN, ...
PROSITE; PSSO231; RICIN B LECTIN; 2.
PROSITE; PSSO275; SHIGA_RICIN; 1.
Glycosidase; Hydrolase, Signal; Toxin.
770017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P02879; 2AAI.
InterPro; IPR00772; Ricin B_lectin.
InterPro; IPR001574; Ricin B_lectin.
Ffam; PF00162; Ricin B_lectin; 6.
Ffam; PF00161; RIP; I.
FRINTS; PR00196; SHIGARICIN.
SWART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
298
564
                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                             Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=28503;
                                                                                                                                                                                                                                                                                                                                                                         RI 183
                                                                                                                                                                                                                                                                                                                                                                                                RV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sambucus ebulus.
                                                                                                                                                                                               72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissum=Leaf;
                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         182
                                                                                                                                                                         Query Match
                                                                                                                                                                                       Best Local
                                                                                                                          NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9AVR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9AVR2
                                                                                                                                                                                                Matches
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MEDLINE=93132798; PubMed=8421313;

A Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;

Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;

Thimary structure of three distinct isoabrins determined by cDNA

Structure of three distinct isoabrins determined by cDNA

T. GATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 289 RRNA.

-!- CATALYTY: BLOMOS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL; M98346; AAA32626.1; -.

EMBL; M98346; AAA32626.1; -.

EMBL; M98346; AAA32626.1; -.

RICHEPPO; IPROO157; RIP.

RESP; PILLAD IABR.

INTERPO; IPROO157; RIP.

REPAIR: PROO161; RIP. I.

REAT: SMO0456; SHIGARICIN.

REAT: SMO0458; RICKN; 2.
                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                        114
                                                                                                                                                                                                                                                                  115 DRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 ELSVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 YPIINFTTAGATVQSYTNFIRAVRGR------LITVLPNRVGLPINQRFILVELSNH 56
                                                                                                                                                       6 QYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSNHA 57
                                                                                                                                                                                                                                  57 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI - - THLFTDVQNRYTFAFGGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TERMBLrel. 01, Last sequence update)
01-MAR-2003 (TERMBLrel. 23, Last annotation update)
Abrin-d (EC 3.2.2.2.2) (rRNA N-glycosidase) (Fragment).
Abrus precatorius (Indian licorice) (Crab's eye).
Bukaryota; Viridiplantae; Streptophtae; Embryophtae; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abrese, Abrus.
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                                                                 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Gaps
        DB 10; Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.8%; Score 318.5; DB 10; Length 528; 43.3%; Pred. No. 7.4e-22; Live 22; Mismatches 69; Indels 15;
Query Match
33.3%; Score 323.5; DB 10; Length
Best Local Similarity 40.0%; Pred. No. 2.7e-22;
Matches 76; Conservative 38; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 AA; 58870 MW; 62ED42FB8FFE60F8 CRC64;
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(TrEMBLrel. 01, Last seq
(TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Best Local Similarity 43.3*
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 IEGEMRTRIR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 IEOEVRRSLO 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996
01-MAR-2003
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SEQUENCE
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Q06076;
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Abrus precatorius (Indian licorice) (Crab's eye).
                                                                                                                                                                                                                                                                                                                                                                                                      NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         094552
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Q945S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
             EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSNHAELSVT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 VSFRLSGATSSSYGVFISNLRKALPYEKKLYDIPLLRSSLSGSQRYALIYLTNYADETIS 84
                                                                                                                                                                                                                                                                                                 Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;
"Trichosanthes kirilowii trichosanthin precursor (TCS) gene.";
submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GIYCOSIDIC BOND AT ONE
                                                                                                                                                                                                              Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids 1, Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                                                             SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AY082348, AAM22782.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.6%; Score 317; DB 10; Length 270; 36.8%; Pred. No. 4.1e-22; ive 45; Mismatches 54; Indels 16
                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (Fragment).
RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 AA; 29683 MW; 531713B754F9B769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 AA.
                                                                                                                            270 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRICHOSANTHIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                 Created)
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Signal; Toxin.
                                                                                                                                                22,
22,
23,
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                                                                                                                            PRELIMINARY;
                                                                                                                                                01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    >270
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                              178 EMRTRIR 184
                                                                   174 RVGVSİR 180
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                              Fragment).
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  118
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Q38760;
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                                                                                                                            Q8LPV7
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                                                                                                      RESULT 12
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ID Q3
AC Q3
DT 01
DT 01
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66 EVGIDVINAYVVAYRAGSQSYFL---RDAPASASTYLFTGTQ-RYSLRFDGSYGDLERWA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS. BELONGS TO TYPE 2 RIP.
-!- SIMILARITY: CAR38654.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 INFITAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                                                                                                                                                                                                           Châins.";
J. Biol. Chem. 266:6848-6852(1991).
J. Biol. Chem. 266:6848-6852(1991).
J. Biol. Chem. 266:6848-6852(1991).
J. Biol. Chem. 266:6848-6852(1991).
J. Biol. Chem. 266:6848-6852(1991).
J. PUNCITON: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION 0.F 608 RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 0F 28 S. RENA. ABRIN-A IS MORE TOXIC THAN RICIN.
J. FUNCITON: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
PRECEDES ENDOCYTOSIS.
                                                                                                                                                                                                                         TISSUB=LEAR;

MEDLINE-19701329; PubMed=2016300;

Byennen G., Mathiesen A., Sundan A.;

"Direct molecular cloning and expression of two distinct abrin A-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Pll14U; LALL.
InterPro; IRPO(1574; RIP.
Print: PR00161; RIP. 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
PROSITE; PS00275; SHIGA RICIN; 1.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.0%; Score 310.5; DB 10; Lengum. 43.2%; Pred. No. 1.6e-21; ... "**mm=rrhes 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       252 AA; 28309 MW; BBFC846B9E92B5DE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q945S2;
01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                              NCBI_TaxID=3816;
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NCBI_TaxID=4202;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY 87
                                                                                                                                                                                               proteins from Sambucus nigra leaves.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-! CATALYIC ACTIVITY: ENDOHYBOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AF409133.;
ALOHIS ALOHIS.1;
InterPro; IPR001774; RIP.
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Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Girbes T., Arias F.J., Antolin P.;
Submitted (MAR-2000) to the MBL/GenBank/DDBJ databases.
EMBL; AF249280; AAN86130.1; -.
Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 YPIINFTTAGATVQSYTNFIRAVR------GRLTVLPNRVGLPINQRFILVELSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Gaps
                                                                                                                                                                         "Characterization and cloning of lectins and ribosome-inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sambucus nigra (European elder).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 31.7%; Score 307.5; DB 10; Length 563; Local Similarity 38.4%; Pred. No. 9.1e-21; Nes 73; Conservative 36; Mismatches 56; Indels 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus;
NCBI_TaxID=4202;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein nigrin 1 precursor (BC 3.2.2.22).
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Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGARICIN; 1.
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                                                                  SEQUENCE FROM N.A.
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                                                                                                                                            Van Damme E.J.M.;
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Best Local Si
Matches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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25; Gaps

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57 AELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFIDVQNRYTFAFGGNY 114
                                                                                                                                   115 DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFOY 174
                                                                                                                                                       88 NGNIVILAVDVINLYVVAFSGNANSYFF----KDATEVQKSNLFVGTKQN-TLSFTGNY 141
                    7 YPIINFTTAGATVOSYTNFIRAVR-----GRLTVLPNRVGLPINQRFILVELSNH 56
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195 IEQEVRRSLQ 204
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930.966 Million cell updates/sec
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2. (SIDSI)gogdata/geneseqy/geneseqp-embl/AA1980.DAT:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Ricin & from offer	Amino acid segment	Ricin A chain In	Richal A-chain	Ricin A-chain ribo	Ricin A-chain RTD	Ciredos A nicia	Semience of Rician	Ricin A encoded by
SUMMARIES	ΠD	AAR30722	AAB19265	AAR37290	AAR63902	AAW25136	AAW21699	AAP70097	AAP70838	AAP95639
	DB	13	21	14	16	18	18	80	8	10
	re Match Length DB I	267	267	267	267	290	290	332	332	332
ا ا ا	Match	100.0	100.0	99.1	99.1	99.1	99.1	99.1	99.1	99.1
	Score	1019	1019	1010	1010	1010	1010	1010	1010	1010
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Anti-cataract immu Ricin D. Ricinus Modified castor be Sequence of Ricinu Castorbean ricin.	bean bean bean of p		Sequence of G-FIT. Ricin A gene produ Ricin A. Syntheti Ricin A chain (RTA Castor oil plant a R. communis agglut Sequence of Ricin	Ricin agglutinin A Trichosanthin anti Amino acid sequenc Synthetic alpha-tr Mature alpha-Trich Trichosanthin (a r Trichosanthin (a r	fr fr pr server
16 AAR70827 10 AAP90079 22 AAG78304 8 AAP70326 18 AAW25787 20 AAY55892	21 AAY78592 22 AAG78301 22 AAG78302 6 AAP50166 22 AAG78300	~ ~ ~	AAR3957 AAR0655 AAR3243 AAR7417 AAW2110 AAP70324	10 AAR95648 21 AAR67359 21 AAR69048 11 AAR07518 13 AAR25573 18 AAW227703	
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ALIGNMENTS

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pH; temperature; cultivation; host; soluble.
              AAR30722 standard; Protein; 267 AA
                                                                                                                                                                                                                       Kara BV;
                                                                                                                                                                                               (ICIL ) IMPERIAL CHEM IND PLC (ZENE ) ZENECA LTD.
                                                                                                                                                                91GB-0003925.
91GB-0003926.
91GB-0004016.
                                                                                                                                                 92EP-0301466.
                                              (updated)
(first entry)
                                                                                                                                                                                                                      Fitton JE, Hockney RC,
                                                                    Ricin A from pICI1102.
                                                                                                                                                                                                                                      WPI; 1992-294124/36.
N-PSDB; AAQ27876.
                                                                                                                                                                26-FEB-1991;
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                                                                                                                 EP501692-A2.
                                            25-MAR-2003
08-FEB-1993
                                                                                                                                 02-SEP-1992
                                                                                                   Synthetic.
                              AAR30722;
RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNYDRLEQLAGRIERIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunotoxin; cytokine; vascular leak syndrome; VLS; lymphoma; myeloma; graft versus host disease; metastatic lesion tumour; tumour; immunotoxin;
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                                                                                                   Prepn. of ricin A comprises cultivating a host, including a DNA sequence which encodes ricin A, e.g. from pICII102, in a nutrient medium for an initial period at a first pH value which favours growth of the host, and cultivation the host for a further period at a pH lower than the first pH value, and opt. cooling the host during the terminal portion of the cultivation and harvesting the host during the the terminal portion. By adjusting the pH and temp, during the cultivation of hosts, high yields of soluble recombinant ricin A
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "vascular leak syndrome (VLS) inducing motif"
   Prepn. of soluble recombinant polypeptide(s), esp. ricin A - by adjusting pH and/or temp. during cultivation to increase yield of soluble prod.
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0
                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1019; DB 13; Length 267; 100.0%; Pred. No. 5.8e-100; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a human ricin toxin A chain (RTA).
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                                                                                                                                                                                                                                                   (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB19265 standard; protein; 267 AA
                                                                           Disclosure, Fig 9; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 FQYIEGEMRTRIRYNRRS 198
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Best Local Similarity 100.0
Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                    267 AA;
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                                                                                                                                                                                                                                   are obtained.
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                                         Modifying the ability of a proteinaceous composition to induce a toxi effect for reducing vascular leak syndrome, comprises identifying at least one specified amino acid sequence and altering it
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                             The specification describes a method for producing immunotoxins and cytokines with a reduced ability to promote vascular leak syndrome (VLS). The immunotoxins are useful for treating graft versus host disease, non-Hodgkin's and Hodgkin's lymphoma, myeloma, metastatic lesson tumours and some type of solid tumours. The present sequence represents an immunotoxin (ricin toxin A chain) which induces VLS. The VLS-inducing motif can be mutated or deleted so that VLS is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Type II ribosome-inactivating protein; type II RIP; gelonin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin.
                                                                                                                                                                                                                                                                                                  100.0%; Score 1019; DB 21; Length 267; 100.0%; Pred. No. S.8e-100; .ive 0; Mismatches 0; Indels 0;
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                                                                                                    Example 1; Page 119-120; 125pp; English.
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                                                                                                                                                                                                                                                                                                                                 198; Conservative
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               WPI; 2000-664922/64.
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                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                       267 AA;
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19-JUN-1992;
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09-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 YDRIEQLAGNIRENIELGNGPLEFAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                      The invention covers analogues of Type I RIPs. Ricin is a Type II RIP whose A chain is homologous to plant type I RIPs. The analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues pref. joined via a disulphide linkage to a molecule which specifically binds to a traget cell, e.g. an antibody fragment. (Updated on 09-JAM-2003 to acorrect PN field.)
                                                                                                                                                                                                                                                                                                                                                                                    3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                   PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
               cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide(s) encoding type I ribosome-inactivating proteins
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Analogues of type I ribosome inactivating protein - useful as
                                                                                                                                                                                                                                                                                                                        99.1%; Score 1010; DB 14; Length 267; 100.0%; Pred. No. 5.2e-99; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carroll SF;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR63902 standard; protein; 267 AA.
                                                              Claim 1; Page 92; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 YIEGEMRTRIRYNRRS 198
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                        196; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                         267 AA;
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27-JUL-1995
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                                                                                                                                                                                                                                                                                         Seguence
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63 SNHAELSVTLALDVTNAYVVGYRACNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize, proRIP, ribosome inactivating protein, alpha; beta subunit, internal linker; Barley Translation Inhibitor; Trichosanthin; Ricin A-chain; Abrin-A A-chain; Saporin; SIT-1; Inffin A; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30; therapeutic toxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                        3 PKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                               AAR63902 is the ricin A chain gene product, it is analogous to the ribosome-inactivating proteins (RIPS) described in AAR63903-R63911.

RIPS are the key components of cytotoxic therapeutic agents (GTAS), which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is
                                                                                                                                                                                                                             desired, such as autoimmune disease, cancer and graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                     99.1%; Score 1010; DB 16; Length 267;
100.0%; Pred. No. 5.2e-99;
ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricin A-chain ribosome inhibitory protein inactive precursor.
 which are suitable for use as components of cytotoxic
                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW25136 standard; Protein; 290 AA.
                                                 Example 3; Fig 1; 221pp; English.
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95US-0378761.
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                therapeutic agents.
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02-DEC-1997
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26-JAN-1995;
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                                                                                                                                                                                                                                                                                                    Seguence
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Hey ID,
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                                                                                                                                        AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
Which was engineered to contain a selectively removable internal peptide
linker sequence separating the alpha and betea units of the RIP. When
separated the two units regain activity and are capable of inactivating
enkaryotic ribosomes and hence preventing protein production. Many
different RIPS may be produced with an internal linker including
maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
Saporin. The RIPs can be used in the construction of therapeutic
toxins targeted to specific cells such as tumour cells via the
attachment of a targeting polypeptide, e.g. a monoclonal antibody.
A further use is in HIV therapy (see US4869903). There is interest
in expressing RIP recombinantly in host eukaryotic cells, because of
the capacity to provide correct post-translational processing. However,
RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
entaryotic cells, they can be recombinantly expressed in such cells and
then converted to active RIP proteins
cup delideath and active RIP proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                             DNA encoding pro-ribosome inactivating proteins - inactive precursors of ribosome inactivating proteins; can be expressed in eukaryotic cells without causing cell death
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                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Score 1010; DB 18; Length 290; 100.0%; Pred. No. 5.8e-99;
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                                                                                                                   Claim 4; Column 91-94; 186pp; English
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152..162
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              Walsh TA;
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(first entry)
              Morgan AER,
                                     WPI; 1997-362934/33
                                                                                                                                                                                                                                                                                                                                                                                                     290 AA;
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Region
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The sequences given in AAW21698-710 represent Ribosome Inactivating Proteins (RIP's), which may be used in the construction of the proteins (RIP's), which may be used in the construction of the proRIP has a selectively removable, internal peptide linker. The proRIP has a selectively removable, internal peptide linker. The precursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidaes activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 288 RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive proRIP proteins make it possible to provide protein possible. The RIP can be used to make cytotoxic conjugates.
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/note= "Position of possible insertion of internal
peptide linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inactive precursor of maize ribosome-inactivating protein - also
chimeric ribosome-inactivating protein precursors containing
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100.0%; Pred. No. 5.8e-99;
iive 0; Mismatches 0;
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95US-0378761.
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Best Local Similarity
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25-MAR-2003
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ID AAP9
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                                                                                                                                                                                                                                                                                                                                63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                   97
                                                                                                                                                                                                                                                                                                               38 PKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                 123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ
                                                                                                                                                                                                                                                                                               3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLJTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
                                                                                                                                                                          N\text{-}terminal\ \text{methionine} free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase
                                                                                                                                                                                                                     Ricin A may be produced in a form which lacks an N-terminal Metusing Met-aminopeptidase from E.coli.
                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                              99.1%; Score 1010; DB 8; Length 332;
100.0%; Pred. No. 7e-99;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                                   Chang SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                    Chang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP70838 standard; protein; 332 AA.
                                                                                                                                                                                                    Disclosure; Fig. 4; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..32
/note="Leader"
                                                                                                                                                                                                                                                                                                                                                                                                   183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                  218 YIEGEMRTRIRYNRRS 233
                                                                                          86US-0860330.
85US-0778414.
                                                                          86EP-0307242.
        Ricin A; Met-aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A protein encoded by pRA123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003 (updated)
18-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                              Matches 196; Conservative
                                                                                                                                   Bauer KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33..302
                                                                                                                                                 WPI; 1987-110172/16.
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                 (CETU ) CETUS CORP.
                                                                                                                                                                                                                                               332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricinus communis.
                        Escherichia coli.
                                                                                                                                                            N-PSDB; AAN70152
                                                                                                                                  Benbassat A,
                                                                                                 20-SEP-1985;
                                                                         19-SEP-1986;
                                                                                         06-MAY-1986;
                                                        22-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plant toxin
                                        EP219237-A.
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP70838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP70838
q
                                                                                                                                                                                                                                                                                                                                 à
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The full-length sequences encoding ricin A (AAN70520), ricin D (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtch using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70522) shows the nucleotide sequences of three plasmids contg. cDNA inserts obtd. by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an AFG start codon and a HindIII site at the beginning of the mature protein (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors contg. the PhoA promoter-operator and leader sequence (AAN70523) and suitable retroregulators.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 YDRLEQIAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 SNHAELSVTIALDVTNAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVIPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8; Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.1%; Score 1010; DB 8; Length 33; 100.0%; Pred. No. 7e-99; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP95639 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 112pp; English.
                               315..332
/note="B-chain"
/note="A-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 YIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                         86EP-0308877.
                                                                                                                                                                                                                                                                                                                           86US-0837583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(updated)
                                                                                                                                                                                                                                                                                                                                                                                                                        CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1987-265177/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAN70519
                                                                                                                                                                                                                                                                                                                                                                                     (CETU ) CETUS
                                                                                                                                                                                                                                                     13-NOV-1986;
                                                                                                                                                                                                                                                                                                                    07-MAR-1986;
                                                                                                                                                                                       23-SEP-1987.
                                                                                                                     EP237676-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP95639;
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AAR70827 standard; Protein; 554 AA.
                                                                                                                                                                                                                                                                                                                                                                         148..166
/label= LINKER
183 YIEGEMRTRIRYNRRS 198
              218 YIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0101329.
                                                                                                                                                      (first entry)
                                                                                                                                                                              Anti-cataract immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                        . 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gould RM, Kelleher PJ,
                                                                                                                                         (updated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ85386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9503828-A1
                                                                                                                                         25-MAR-2003
                                                                                                                                                      31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-1995.
                                                                                                                                                                                                                                                       Synthetic
                                                                                                               AAR70827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                           AAR7082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant vectors expressing ricin chains or diphtheria toxin -used for prodn. of new immunotoxin conjugates with monoclonal antibodies, having high cell specificity and good extracellular stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDARAITHLFTDVQNRYTFAFGGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain. Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                          Kaplan D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.1%; Score 1010; DB 10; Length 332; 100.0%; Pred. No. 7e-99; 1ve 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                      Greenfield L, Nitecki D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                            Plasmid pRA123; ricin-A; ricin-B; cytotoxicity
                  Ricin A encoded by insert from plasmid pRA123
                                                                                                                         1..35
/label= leader sequence
                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 14; 54pp, English.
                                                                                                                                                  /label=A-chain
303..314
                                                                                                                                                                                                                                                                                                                                                                                                                       Lawyer FC, Horn G,
                                                                                                                                                                                                   315..332
/label=B-chain
                                                                                                                                                                            303..314
/label=linker
                                                                                                                                                                                                                                                                                                                 84US-0578115.
84US-0578121.
84US-0578122.
84US-0648759.
                                                                                                                                                                                                                                                                                          89EP-0201162.
                                                                                                                                                                                                                                                                                                                                                                   84US-0653515
                                                                                                                                                                                                                                                                                                                                                                                             CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1989-286959/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        332 AA;
                                                                     Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAN91281
                                                                                                                                                                                                                                                                                                                                                                                            (CETU ) CETUS
                                                                                                                                                                                                                                                                                         19-JAN-1989;
                                                                                                                                                                                                                                                                                                                             08-FEB-1984;
09-FEB-1984;
                                                                                                                                                                                                                                                                                                                 08-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                        07-SEP-1984;
                                                                                                                                                                                                                                                                                                                                                                   20-SEP-1984;
                                                                                                                                                                                                                                                               04-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nost cells.
                                                                                                                                                                                                                                       EP335476-A.
                                                                                                                                                                                                                                                                                                                                                                                                                      Gelfand D,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Piatak MJ;
                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                     Peptide
                                                                                                                                                                         Peptide
                                                                                                                                                                                                 Peptide
                                                                                                                                               Peptide
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The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the immunotoxin was expressed from pHB19 in E. coli. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Immunotoxin; heavy chain; light chain; variable region; antibody;
ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
pHB19; 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 99.1%; Score 1010; DB 16; Best Local Similarity 100.0%; Pred. No. 1.4e-98; Matches 196; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                           note= "MAb 4197X heavy chain"
                                                                                                                                                                                                                    1..27
/label= Sig peptide
/note= "phoA signal sequence"
/label= HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= LIGHT
/note= "MAb 419X light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wood MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      549..554
/label= TAG
/note= "hexa-histidine tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wallace TL,
                                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Fig.4; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= RICIN-A
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63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEALTHLFTDVQNRYTFAFGGN 122
                                                              123 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIIGIQMISEAARFQ 182
                                                                                                                 3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of DNA from Ricinu communis, Zamibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                      Ricin D; Ricinus communis; caster beans; Zanibariensis variety; modified; lectin binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.1%; Score 1010; DB 10; Length 562; 100.0%; Pred. No. 1.4e-98; of Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B chain is removed or diminished to reduce cell binding.
                                                                                                                                                                                                                                       AAP90079 standard; protein; 562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; fig 1; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                            Ricinus communis (caster beans).
                                                                                                                                                  183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                          460 YIEGEMRTRIRYNRRS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87US-0124735
                                                                                                                                                                                                                                                                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1989-178366/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jones S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAN90068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-NOV-1987;
                                                                                                                                                                                                                                                                                        25-MAR-2003
                                                                                                                                                                                                                                                                                                      01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                    WO8904839-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown EL,
                                                                                                                                                                                                                                                                 AAP90079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                               Ricin D.
                                                                                                                                                                                                                            AAP90079
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98 SNHABLSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYFFAFGGN 157
                                         123 YDRLEQLAGNLRENIELGNGPLEEALSALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                   158 YDKLEQLAGNIENIELGNGPLEEAISALYYYSTGGTQLPTLAKSFIICIQMISEAARFQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence relates to the amino acid sequence of a modified preproricin protein encoded by AAI64145. The invention relates to a novel toxin (e.g. ricin) based antiviral agent which is toxic to virus-infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Proricin consists of the ricin A chain, a linker peptide, and the ricin B chain. Proricin is proteclytically cleaved between the A chain and the linker to yield mature ricin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Ricin_B_chain
/note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                              Castor bean plant, preproricin, ricin; A chain, B chain, human immunodeficiency virus infection, HIV; toxin, antiviral agent, retroviral infection, anti-HIV; virucide, viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             796..297
/label= HIV_protease_cleavage_site
304..565
                                                                                                                                                                                                                                                                                                                                                                      Chimeric - Ricinus communis
Chimeric - Human immunodeficiency virus type 2.
                                                                                                                                                                                                                                                                                  Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Linker_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "N-glycosidase"
292..303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= Ricin A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 59-63; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                  AAG78304 standard; Protein; 565 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          25..565
/label= Proricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                    218 YIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-FEB-2000; 2000US-0182759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-FEB-2001; 2001WO-US05282.
                                                                                                    183 YIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Keener WK, Ward TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-581908/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAI64145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200160393-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage-site
                                                                                                                                                                                                                                                         27-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2001
                                                                                                                                                                                                                              AAG78304;
                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                      RESULT 12
AAG78304
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0; Gaps

62

63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122

PICTION PETAGATVOSYTNEIRAVRGRETTGADVRHEIPVEPPRVGEPINVERFILVEL 97

38

3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL

196; Conservative

Matches

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Similarity

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us-10-083-336a-7.rag

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                                                                                                                                                                                                                                                                                                                                                                  123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                    SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
cells, but non-toxic to uninfected cells. The invention has anti-HIV and rurucide activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the problem of the problem and effectively preventing the latency/rebound problem.
                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                         86
                                                                                                                                                                                                                                                                                                                  27 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                           PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                    .,
0
                                                                                                                                                                                                                                    99.1%; Score 1010; DB 22; Length 565; 100.0%; Pred. No. 1.4e-98; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hence of Ricinus communis (castor bean) Ricin toxin or ricin) E precursor encoded by pRT38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP70326 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "B-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 YIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86EP-0308877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86US-0837583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315..576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36..302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CETU ) CETUS CORP. (CHIR ) CHIRON CORP.
                                                                                                                                                                                                          565 AA;
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant toxin.
                                                                                                                                                                                                                                                            Matches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP70326;
                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                 problem.
                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
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The full length sequences encoding ricin A (AAN70520), ricin D (AAN70525) putative ricin E (AAN70526) and RCA (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtained, using the messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The Library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70521), AAN70521), Shows the nucleotide sequences of three plasmids containing cDNA inserts obtained by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a HindIII site at the beginning of the mature protein, (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors containing the PDNA promoter-operator and leader sequence (AAN70533) and sultable retroregulators.

("Dedated on 25-MAR-2003 to correct PA field.)
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNHABLSVTLALDVTNAXVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLFTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                    New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricin, cytotoxin, hybrid protein, cell delivery, cell binding ligand; translocation domain; diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1010; DB 8; Length 576; Pred. No. 1.5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No.
                                                                                                                                                                              Disclosure; Fig 14(1-2); 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW25787 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36..302
/label= A-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 YIEGEMRTRIRYNRKS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.C
Marches 196; Conservative
                                                                                                                                          purer and soluble prods.
                                                 WPI; 1987-265177/38.
N-PSDB; AAN70526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Castorbean ricin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
               Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW25787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
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218 YIEGEMRTRIRYNRRS 233

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This polypeptide comprises the castorbean cytotoxin, ricin.

DNA (see AAT91638) encoding the enzymatic A domain and a portion of the A-to-B linker peptide of ricin was used to construct a ricin-diphtheria toxin B-interleukin-2 gene that was expressed in ricin-diphtheria toxin B-interleukin-2 gene that was expressed in E. coli. The hybrid protein can be isolated and used to treat conditions involving over-production of cells bearing IL2 receptors, such as certain 7-cell lymphomas and organ transplant rejection crises. The hybrid inactivates ribosomes in cells bearing IL2 receptors, resulting in cessation of protein synthesis and death of target cells. Claimed hybrid proteins comprise a translocation of comain and a cell binding domain from e.g. a hormone, growth factor or polypeptide toxin. The hybrid molecules can be used for the delivery of agents (e.g. therapeutic genes toxins, detectable cor polypeptide toxin. The hybrid molecules can be used for the targeted cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a high broportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a high broportion of the precise control of composition.

Consistency, and the precise control of composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hybrid molecules for delivery of agents to cells - comprise a binding domain of a cell binding ligand and a portion of a translocation domain of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.1%; Score 1010; DB 18; Length 576;
100.0%; Pred. No. 1.5e-98;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 11A-B; 30pp; English.
                                    315..576
/label= B-domain
    303..314
/label= Linker
                                                                                                                                                                                                                              84US-0618199.
85US-0726808.
85US-0742554.
89US-0456095.
90US-0538276.
                                                                                                                                                                         93US-0102387.
                                                                                                                                                                                                                91US-0722484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
les 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-470103/43.
                                                                                                                                                                                                                                                                                                                                                                   (SERA-) SERAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT91638
                                                                                                                                                                       04-AUG-1993;
                                                                                              US5668255-A
                                                                                                                                                                                                                                07-JUN-1984
                                                                                                                                   16-SEP-1997
                                                                                                                                                                                                                                                    25-APR-1985
                                                                                                                                                                                                                                                                      07-JUN-1985
                                                                                                                                                                                                                                                                                        22-DEC-1989
                                                                                                                                                                                                                                                                                                          14-JUN-1990
                                                                                                                                                                                                                                                                                                                               04-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                         Murphy JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Peptide
                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Recombinant, hybrid, binding domain, ligand, animal cell, diphtheria, translocation domain, botulinum, neurotoxin, ricin, cholera, tetanus, shiga-like toxin; pertussis, translocation, cytoplasmic membrane, HIV, cytosol, therapy, genetic deficiency disease, enzyme; co-factor; poison, adipocyte, cancer; virus; infection, antibody.
                                                                                                                                                                                                                                                                                                                                                Recombinant DNA molecule encoding a three part hybrid protein used in the treatment of Aids and genetic deficiency diseases -
                AAY55892 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                          Example 4; Fig 11; 31pp; English.
                                                                                                                                                                                                                      84US-0618199
91US-0722484.
85US-0726808.
85US-0742554.
89US-0456095.
                                                                                                                                                                                              95US-0488246,
                                                                                                                                                                                                                93US-0102387
                                                   15-FEB-2000 (first entry)
                                                                     Castor bean ricin toxin.
                                                                                                                                                                                                                                                                                     (SERA-) SERAGEN INC.
                                                                                                                                                                                                                                                                                                                       WPI; 1999-632431/54.
                                                                                                                                          Ricinus communis.
                                                                                                                                                                                                                                                                                                                                N-PSDB; AAZ30663.
                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                          US5965406-A.
                                                                                                                                                                                                                         1984;
                                                                                                                                                                                                                04-AUG-1993;
                                                                                                                                                                                                                                                         22-DEC-1989;
                                                                                                                                                                                                                                        25-APR-1985
                                                                                                                                                                                                                                                 07-JUN-1985
                                                                                                                                                                                                                                                                                                                                               Recombinant
                                                                                                                                                                            12-0CT-1999
                                                                                                                                                                                                                               27-JUN-1991
                                                                                                                                                                                                                                                                                                      Murphy JR;
                                  AAY55892;
                                                                                                                                                                                                                        -NUL-10
RESULT 15
         AAY55892
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The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein cours, bridge-like toxin, pertussis toxin and tetanus coxin, which translocate the third part of the across the cytoplasmic coxin, which translocate the third part of the across the cytoplasmic commitment into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the castor bean ricin toxin sequence for use in generating the hybrid of the invention. The hybrid molecule enables the direction properly and convention of the hybrid is sepecially used in treating calleviate or cure the disease. The hybrid is sepecially used in treating cupylying the missing function, to supplementing celluar levels of a particular enzyme or a scarce precursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as cell, or viral proteins or viral proteins. It is also detectable labels into cells.

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SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGN 122 98 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 157 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182

63

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183 YIEGEMRTRIRYNRRS 198

Search completed: February 10, 2004, 16:22:27 Job time: 33.7583 secs

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                                                            February 10, 2004, 16:18:30; Search time 11.4485 Seconds (without alignments) 731.761 Million cell updates/sec
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1 MVPKQYPIINFTTAGATVQS.....ARFQYIEGEMRTRIRYNRRS 198
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-07-938-731-1

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US-08-425-336-1

US-08-446-360-1

US-08-446-360-1

US-08-446-360-1

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US-09-136-389-1

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US-08-356-786-10

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US-08-36-36-6

US-08-389-16-7

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US-08-646-389-6

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                                                                                                                                                                               328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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3 4 4 4 4 5 5 5 5 5 5 5 5 5			Length Indels
28 342 33.6 267 1 US-08-485-286-74 29 342 33.6 289 1 US-07-923-692C-4 31 342 33.6 289 1 US-08-1842-920-4 32 342 33.6 289 1 US-08-1842-920-4 33 342 33.6 289 3 US-08-482-920-4 34 342 33.6 289 3 US-08-483-502-4 35 342 33.6 289 3 US-08-483-502-4 35 341.5 33.5 289 1 US-08-378-701-7 37 329.5 32.3 250 1 US-08-378-761A-71 38 323.5 32.3 250 1 US-08-378-761A-71 38 323.5 31.7 25.5 1 US-08-378-33-3 312.5 30.7 25.5 1 US-08-485-33-6 41 312.5 30.7 25.5 1 US-08-485-33-6 42 312.5 30.7 25.5 1 US-08-485-33-6 43 312 30.6 248 3 US-08-248-7 45 312 30.6 290 2 US-08-245-754A-2	ALIGNMENTS	RESULT 1 US-08-218-303-16 Sequence 16, Application US/08218303 Sequence 16, Application US/08218303 Sequence 16, Application US/08218303 Sequence 16, Application US/08218303 Sequence 10, Object C. APPLICANT: Britch Condense C. TITLE OF INVENTION: FERRENTATION PROCESS CORRESPONDENCE ADDRESS: 23 CORRESPONDENCE ADDRESS: ADDRESSE: Cushman, Darby & Cushman STREET: 1615 L Street, N.W. STREET: 1615 L Street, N.W. CITY: Washington STREET: D.C. COUNTRY: U.S.A. ZIP: 20036-5601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Ploppy disk COMPUTER READABLE FORM: MEDIUM TYPE: PLODS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/218,303 FILING DATE: 26-FEB-1992 ATTOREY/ASTE TOWNER: US/08/218,303 FILING DATE: 26-FEB-1992 ATTOREY/ASTE TOWNER: PRICATION NUMBE: ROALIS, PAUL RESERRENCE/DOCKET NUMBER: PRICATION TELEPAX: 202-822-0944 TELERAX: 202-822-0944 TELERAX: 207-822-0944 TELERAX: 207-822-0944 TUPPE: amino acids TYPE: amino acids TYPE: Anino acid TOPOLOGY: linear MOLECULE TYPE: protein	Query Match 100.0%; Score 1019; DB 1; Best Local Similarity 100.0%; Pred. No. 1.3e-111; Matches 198; Conservative 0; Mismatches 0;

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1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60

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GENERAL INCORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: VITETTA, ELLEN S.
APPLICANT: VITETTA, ELLEN S.
APPLICANT: SALLASHAW, JOAN
APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: BALUNA; GOALASHAW, JOAN
APPLICANT: BALUNA; ROXANA G.
TITLE OF INVENTION: SYNDROME (VLS)
TITLE OF INVENTION: SYNDROME (VLS)
FILE REFREENCE: UTSD:603
CURRENT FILING DATE: 2000-03-30
CURRENT FILING DATE: 1999-03-30
EARLIER APPLICATION NUMBER: 60/126,826
EARLIER APPLICATION NUMBER: 60/126,826
EARLIER FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                              121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                       61 ELSNHABELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEA1THLFTDVQNRYTFAFG 120
                                                                                               121 GNYDRLEQLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
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100.0%; Score 1019; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 198; Conservative 0; Mismatches 0;
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Patent No. 6566500
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          181 FOYIEGEMRTRIRYNRRS 198
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1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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Best Local Similarity 100.0%; Score 1019; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.3e-111;
Matches 198; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 2005-3918
COMPUTER READABLE FORM:
MEDING TYPE: Diskette, 3.50 inch, 1.44 MB storage COMPUTER: IBM PC/XI/AI Compatibles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:

COMPUTER:

COMPUTER:

OPERATING SYSTEM:

MS-DOS

SOFTWARE:

MICTOSOFT Word or ASCII editors

SOFTWARE:

APPLICATION DATE:

APPLICATION NUMBER:

CLASSIFICATION NUMBER:

BRION APPLICATION NUMBER:

APPLICATION NUMBER:

O1/842,081

FILING DATE:

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FILING DATE:

CLASSIFICATION NUMBER:

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REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: DJB/9901/215431/TGM
TELEDHONICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEPHONE: 202-822-0944
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S: INTELLECTUAL PROPERTY GROUP OF
S: PILLSBURY MADISON & SUTRO, L.L.P.
1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 61, Application US/08338793D
Patent No. 5840521
GENERAL INFORMATION:
APPLICANT: Barth, Peter Thomas
                                                                                                                                                                                                                                                                                                                                                     181 FOYIEGEMRIRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                181 FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Barth, Peter Thomas
TITLE OF INVENTION: VECTOR
NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 6714627 CUSH INFORMATION FOR SEQ ID NO: 61: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: Sir
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us-10-083-336a-7.rai

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ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
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                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                    Bicknel]
                                                                                  CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                   60603
                                  ADDRESSEE:
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APPLICANT: Carroll, Stephen F.
APPLICANT: Let, Julie A.
APPLICANT: Let, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                           STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         FILING DATE: 19920619
CLASSIFICATION: 435
PRIOR APPLICATION DATA;
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5376546and, Greea E.
RECISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-5750
TELEFACOMORPHORES: 25-3856
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
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Patent No. 5416202
GENERAL INFORMATION:
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F
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AMINO ACID
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Best Local Similarity 100.(
Matches 196; Conservative
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                                                                                                        Chicago
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                                                                                                                                                     COUNTRY:
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US-07-988-430-1
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63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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Sequence 1, Application US/08425336
Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
99.1%; Score 1010; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
CLASSIPICATION: 435
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION: DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-7UN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 35302
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REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 31333
TELEPHONE: (312) 346-5750
STREET: Two First National Plaza, 20 South Clark
STREET: Street
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63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF SEQUENCES: 169
CORRESPONDENCE ADDRESS: 169
ADDRESSEE: MCANDAREWS, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
99.1%; Score 1010; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0; Indels
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
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500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                        PRICE APPLICATION DATA:
APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: 05 07/901,707
FILING DATE: 19-UDN-1992
PRICE APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MSYERS, THOMAS C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
FELECOMMUNICATION INFORMATION:
THE DECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5744580
GENERAL INFORMATION:
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
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                                                      Illinois
                                                                                                       60606-6402
                           Chicago
                                                                            COUNTRY:
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63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGN 122
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                                                                                               11022US07/200-70.P3.C2A
                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 575659
GENERAL INFORMATION
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                               ILEMERAX: 312/707-8889
TELEX: 650 388-1248
INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 267 amin
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8989
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amino acid
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Matches 196; Conservative
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                                                     COMPUTER READABLE FORM:
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Chicago
                           USA
                                                              MEDIUM TYPE:
                                       60661
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US-08-477-484B-1
                           COUNTRY:
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